

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:38:46 ; Search time 70 Seconds
(without alignments)
171.343 Million cell updates/sec

Title: US-10-664-605-5
Perfect score: 68
Sequence: 1 CFGXXXDRIGXXSXXGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	83.8	106	2 Q6VYM3	BRABE
2	57	83.8	142	1 ANF_ACITR	
3	57	83.8	146	2 Q7T217	ONCMY
4	57	83.8	148	2 Q78AW6	SALSA
5	57	83.8	152	2 Q9YGJ1	SALSA
6	56	82.4	30	1 ANF_RANRI	
7	56	82.4	83	2 Q4TD23	TETNG
8	56	82.4	128	1 ANF_CAVPO	
9	56	82.4	133	1 ANFB_FUGRU	
10	56	82.4	138	1 ANFB_OREMO	
11	56	82.4	138	2 Q4T953	TETNG
12	56	82.4	139	1 ANF_FUGRU	
13	56	82.4	140	1 ANF_OREMO	
14	56	82.4	145	1 ANF_RANCA	
15	56	82.4	145	2 Q5XPR8	RANRI
16	56	82.4	146	2 Q7T1Q2	ORYLA
17	56	82.4	150	1 ANFB_ACITR	
18	56	82.4	159	2 Q90X61	BUFWA
19	55	80.9	22	1 ANFC_CHICK	
20	55	80.9	25	2 Q4SND6	TETNG
21	55	80.9	27	1 ANF_ANGJA	
22	55	80.9	33	2 Q9QZ96	CAVPO
23	55	80.9	37	1 NFN_PSEPC	
24	55	80.9	38	2 Q7LZ09	VIPLE
25	55	80.9	101	2 Q4S797	TETNG
26	55	80.9	103	1 ANFB_BOVIN	
27	55	80.9	112	2 Q9GLK5	FELCA
28	55	80.9	115	1 ANFC_SCYCA	
29	55	80.9	118	1 ANFD_RANCA	
30	55	80.9	120	1 ANFC4_FUGRU	
31	55	80.9	121	1 ANFB_MOUSE	

32	55	80.9	121	1 ANFB_RAT		P13205	rattus norv
33	55	80.9	121	1 ANFC4_ORYLA		Q80017	oryzias lat
34	55	80.9	121	2 Q794A8	MUSE	Q794a8	mus musculu
35	55	80.9	121	2 Q91V40	MUSSE	Q91v40	mus spicile
36	55	80.9	121	2 Q54AE9	MUSE	Q54ae9	mus musculu
37	55	80.9	121	2 Q55086	MUSE	Q55086	mus musculu
38	55	80.9	126	1 ANFC1_FUGRU		Q805d6	fugu rubrip
39	55	80.9	126	1 ANFC2_ORYLA		Q8ayr5	oryzias lat
40	55	80.9	126	1 ANFC_BOVIN		P55206	bos taurus
41	55	80.9	126	1 ANFC_HUMAN		P23582	homo sapien
42	55	80.9	126	1 ANFC_MOUSE		Q61839	mus musculu
43	55	80.9	126	1 ANFC_PIG		P18104	sus scrofa
44	55	80.9	126	1 ANFC_RAT		P55207	rattus norv
45	55	80.9	126	1 ANFC_SHEEP		P56283	ovis aries
46	55	80.9	126	2 Q4ZG41	HUMAN	Q4zg41	homo sapien
47	55	80.9	126	2 Q544K5	MUSE	Q544k5	mus musculu
48	55	80.9	129	1 ANFB_SHEEP		Q46541	ovis aries
49	55	80.9	129	1 ANFC_RANCA		P20968	rana catesb
50	55	80.9	130	1 ANFC2_FUGRU		Q805d5	fugu rubrip
51	55	80.9	131	1 ANFB_PIG		P07634	sus scrofa
52	55	80.9	131	1 ANFC1_ONCMY		Q8axr3	oncorhynch
53	55	80.9	131	1 ANFC1_ORYLA		Q8ayr6	oryzias lat
54	55	80.9	131	1 ANFC2_ONCMY		Q8axr2	oncorhynch
55	55	80.9	131	1 ANFC_ANGJA		P18145	anguilla ja
56	55	80.9	131	2 Q805E7	OREMO	Q805e7	oreochromis
57	55	80.9	132	2 Q6L7Z3	CAMDR	Q9GLk4	felis silve
58	55	80.9	132	1 ANFC_FELCA		Q617z3	camelus dro
59	55	80.9	135	1 ANFC_SQUAC		P41319	squalus aca
60	55	80.9	136	1 ANFC_TRISC		P55208	triakis scy
61	55	80.9	140	1 ANFB_CANFA		P16859	canis fami1
62	55	80.9	140	1 ANF_CHICK		P18908	gallus gall
63	55	80.9	140	2 Q9PSV1	ANGJA	Q9psv1	anguilla ja
64	55	80.9	144	2 Q805E6	FUNHE	Q805e6	fundulus he
65	55	80.9	147	2 Q8VHG9	NOTAL	Q8vhg9	notomys ale
66	55	80.9	147	2 Q9DGK8	XENLA	Q9dgk8	xenopus lae
67	55	80.9	149	1 ANF_CANFA		P07499	canis fami1
68	55	80.9	150	1 ANFC_ACITR		Q76kw6	acipenser t
69	55	80.9	150	1 ANFV_ANGJA		P22642	anguilla ja
70	55	80.9	150	1 ANF_PIG		P24259	sus scrofa
71	55	80.9	151	2 Q5JZE1	HUMAN	Q5jze1	homo sapien
72	55	80.9	152	1 ANF_MOUSE		P07501	bos taurus
73	55	80.9	152	1 ANF_RAT		P05125	mus musculu
74	55	80.9	152	1 ANF_SHEEP		P01161	rattus norv
75	55	80.9	152	2 Q6L7Z4	CAMDR	Q6L7z4	camelus dro
76	55	80.9	152	2 Q9TQW1	BALPH	Q9tqw1	balaenopter
77	55	80.9	152	2 Q5FW59	MUSE	Q5fw59	mus musculu
78	55	80.9	152	2 Q8VHH2	NOTAL	Q8vhh2	notomys ale
79	55	80.9	153	1 ANF_FELCA		Q9gl04	felis silve
80	55	80.9	153	1 ANF_HORSE		P27104	equus cabal
81	55	80.9	153	1 ANF_HUMAN		P01160	homo sapien
82	55	80.9	153	1 ANF_RABIT		P07500	oryctolagus
83	55	80.9	155	2 Q29130	TUPGB	Q29130	tupaia glis
84	55	80.9	181	2 Q90Y11	CRODU	Q90y11	crotalus du
85	55	80.9	181	2 Q90Y12	CRODU	Q90y12	crotalus du
86	55	80.9	221	2 Q6LEM5	BOTJA	Q6lem5	bothrops ja
87	55	80.9	256	2 Q9PT52	AGKHA	Q9pt52	agkistrodon
88	55	80.9	263	2 Q8QG91	BOTJA	Q8qg91	bothrops in
89	55	80.9	265	2 Q9PW56	BOTJA	Q9pw56	bothrops ja
90	55	80.9	277	2 Q4TBD2	TETNG	Q4tbd2	tetraodon n
91	55	80.9	39	1 VNOC_OXYMI		P83230	oxyuranus m
92	54	79.4	39	1 VNOC_OXYSA		P83231	oxyuranus s
93	54	79.4	104	2 Q6DR58	XENLA	Q6df58	xenopus lae
94	54	79.4	162	2 Q7YZU5	EPTBU	Q7yzu5	eptatretus
95	53	77.9	112	1 ANFC3_ORYLA		Q80018	oryzias lat
96	53	75.0	145	1 ANFV_ACITR		P83962	acipenser t
97	51	75.0	35	2 Q9PRU2	ONCMY	Q9pru2	oncorhynch
98	50	73.5	134	1 ANFB_HUMAN		P16860	homo sapien
99	50	73.5	134	2 Q6FGY0	HUMAN	Q6fgy0	homo sapien
100	50	73.5	149	2 Q7T216	ONCMY	Q7t216	oncorhynch
101	50	73.5	35	1 VNQA_OXYMI		P83224	oxyuranus m
102	49	72.1	35	1 VNQA_OXYSA		P83226	oxyuranus s
103	49	72.1					
104	49	72.1					

105	49	72.1	35	1	VNOA_OXYSC	P83225 oxyuranus s	178	33.5	49.3	178	2	O8MLP4_DROME	O8mlp4 drosophila
106	49	72.1	35	1	VNOB_OXYMI	P83227 oxyuranus m	179		49.3	369	1	VP6_AHSV6	O64913 african hor
107	49	72.1	35	1	VNOB_OXYSA	P83229 oxyuranus s	180	33	48.5	96	2	O5BSC0_SCHJA	O5bsc0 schistosoma
108	49	72.1	35	1	VNOB_OXYSC	P83228 oxyuranus s	181	33	48.5	137	2	O97IW5_CLOAB	O97iws clostridium
109	48	72.1	111	2	Q4VR12_OXYSC	Q4vr12 oxyuranus s	182	33	48.5	241	2	O5PT75_AZOSE	O5p7a5 azoarcus sp
110	48	70.6	38	2	DNP_DENAN	P28374 dendroaspis	183	33	48.5	408	2	O8H1G9_ARATH	O8h1g9 arabidopsis
111	48	70.6	53	2	O8QGP7_DENAN	O8qgp7 dendroaspis	184	33	48.5	419	2	O9M0H3_ARATH	O9m0h3 arabidopsis
112	48	70.6	137	2	O5Y820_XENIA	O5y820 xenopus lae	185	33	48.5	441	2	O8MRP5_BRAJA	O8mrp5 bradyrhizob
113	47	69.1	128	2	Q4T954_TETNG	Q4t954 tetraodon n	186	33	48.5	454	2	O6KKP4_BDEBA	O6mkp4 bdellovibri
114	47	69.1	158	1	ANFC3_FUGRU	Q805d4 fugu rubrip	187	33	48.5	472	1	E1BL_ADE41	P10546 human adeno
115	46	67.6	111	2	O8HXV3_SAGOE	Q8hvx3 saguinus oe	188	33	48.5	476	1	E1BL_ADE40	P10545 human adeno
116	46	67.6	111	2	O8HXV4_9PRIM	Q8hvx4 macaca sp.	189	33	48.5	505	2	Q7XSK0_ORYSA	O7xsk0 oryza sativ
117	46	67.6	111	2	O8HXV5_PONPY	Q8hvx5 pongo pygma	190	33	48.5	539	2	O84VI7_HORVD	O84vi7 hordium vul
118	46	67.6	111	2	O8HXV6_9PRIM	Q8hvx6 gorilla gor	191	33	48.5	558	2	O88JS8_PSEPK	O88js8 pseudomonas
119	46	67.6	111	2	O8HXV7_PANTR	Q8hvx7 pan troglod	192	33	48.5	567	2	O8Y1Z0_RALSO	O8y1z0 ralstonia s
120	46	67.6	126	2	Q9D288_MOUSE	Q9d288 mus musculu	193	33	48.5	585	2	O8IB78_PLAF7	Q8ib78 plasmodium
121	45	66.2	139	2	P79799_MICCO	P79799 micrurus co	194	33	48.5	1763	2	O4HX73_GIBZE	Q4hx73 gibberella
122	42	61.8	740	2	Q5Z8V2_ORYSA	Q5z8v2 oryza sativ	195	33	48.5	2544	2	O4LY33_9BURK	Q4ly33 burkholderi
123	39	57.4	33	2	Q9GLD8_FELCA	Q9glD8 felis silve	196	32.5	47.8	563	2	O5ZY26_9TRYP	O5zy26 trypanosoma
124	39	57.4	181	2	Q61IG5_DROME	Q61ig5 drosophila	197	32	47.8	762	2	O61693_CAEBL	O61693 caenorhabdi
125	39	57.4	216	2	Q7SXM9_BRARE	Q7sxm9 brachydanio	198	32	47.1	66	2	O07037_PSEAE	O07037 pseudomonas
126	38	55.9	918	2	Q4WHV9_ASPEU	Q4whv9 aspergillus	199	32	47.1	132	2	O07037_PSEAE	O07037 pseudomonas
127	37	54.4	407	2	O8EET6_SHEON	Q8eet6 shewanella	200	32	47.1	196	1	COAE_LEPIC	O72mv4 leptospira
128	37	54.4	1067	2	O01419_BOMMO	O01419 bombyx mori	201	32	47.1	196	1	COAE_LEPIN	O8ezj0 leptospira
129	36	52.9	420	2	Q7UNA6_RHOBA	Q7una6 rhodopirell	202	32	47.1	211	2	Q7RFH9_PLAYO	Q7rfh9 plasmodium
130	36	52.9	519	2	Q6NUB3_XENIA	Q6nub3 xenopus lae	203	32	47.1	233	2	O5C1X3_SCHJA	O5c1x3 schistosoma
131	36	52.9	541	2	Q9Z5A6_STRCO	Q9z5a6 streptomyce	204	32	47.1	260	2	Q94AV8_ARATH	O94av8 arabidopsis
132	36	52.9	1076	2	O868Q4_BOMMO	Q868q4 bombyx mori	205	32	47.1	262	2	O5V399_HALMA	O5v399 halocarcula
133	35	51.5	53	2	O8CLV0_YERPE	Q8clv0 yerisia pe	206	32	47.1	273	2	O5UP43_MIMIV	O5up43 mimivirus.
134	35	51.5	113	2	Q08321_YEAST	Q08321 saccharomyc	207	32	47.1	274	2	O9ZXAI_BPPHC	O9zxai bacteriopho
135	35	51.5	202	2	O5AG45_CANAL	Q5ag45 candida alb	208	32	47.1	275	2	O4FKD0_9TRYP	Q4fkD0 leptospira
136	35	51.5	222	2	Q4SI88_TETNG	Q4si88 tetraodon n	209	32	47.1	280	2	O5BFY3_EMENI	Q7rfh9 plasmodium
137	35	51.5	426	2	Q6DIC6_ERWCT	Q6dic6 erwinia car	210	32	47.1	297	2	O8R5M0_MOUSE	O5cix3 schistosoma
138	35	51.5	449	2	Q63L30_BURPS	Q63l30 burkholderi	211	32	47.1	312	2	O8TF64_HUMAN	O94av8 arabidopsis
139	35	51.5	456	2	Q4ITI9_AZOV1	Q4iti9 azotobacter	212	32	47.1	314	2	Q4TH97_TETNG	O5v399 halocarcula
140	35	51.5	487	2	Q4LKC2_9BURK	Q4lkc2 burkholderi	213	32	47.1	347	2	O75227_HUMAN	O5up43 mimivirus.
141	35	51.5	540	2	Q82LI0_STRAW	Q82li0 streptomyce	214	32	47.1	380	2	O8A110_BACTN	O9zxai bacteriopho
142	35	51.5	1053	2	Q8MY27_9NEOP	Q8my27 papilio xut	215	32	47.1	393	2	Q749J8_GEOSL	Q8ezj0 leptospira
143	35	51.5	1053	2	Q8MY35_9NEOP	Q8my35 papilio xut	216	32	47.1	399	2	Q4NJU5_9MICC	O7rfh9 plasmodium
144	35	51.5	1053	2	Q8MY31_9NEOP	Q8my31 papilio xut	217	32	47.1	405	2	Q64BC2_9ARCH	O5cix3 schistosoma
145	35	51.5	1053	2	Q8MY33_9NEOP	Q8my33 papilio xut	218	32	47.1	408	2	O8FVK9_BRUSU	O94av8 arabidopsis
146	35	51.5	1336	2	Q73WQ7_MYCPA	Q73wg7 mycobacteri	219	32	47.1	410	2	O5V6A3_HALMA	O5v399 halocarcula
147	35	51.5	1351	2	Q9AV94_SOYBN	Q9av94 glycine max	220	32	47.1	411	2	Q9A961_CAUCR	O5v6a3 halocarcula
148	35	51.5	2111	1	MCAS_MYCBO	Q02251 mycobacteri	221	32	47.1	413	2	O8BGB4_POUSE	O9a961 caulobacter
149	35	51.5	2111	2	P96291_MYCTU	P96291 mycobacteri	222	32	47.1	419	2	O5R9N7_PONPY	Q8bgb4 m mus muscu
150	35	51.5	2116	2	Q9CD78_MYCLE	Q9cd78 mycobacteri	223	32	47.1	424	2	O82XZ0_NITTEU	O5r9n7 pongo pygma
151	35	51.5	2118	2	Q49624_MYCLE	Q49624 mycobacteri	224	32	47.1	428	2	O5ZWC2_LEGPH	Q82xz0 nitrosomona
152	35	51.5	4723	2	Q86BA1_DROME	Q86ba1 drosophila	225	32	47.1	428	2	O5X605_LEGPA	O5zwc2 legionella
153	34	50.0	56	2	Q9FCV7_LISMO	Q9fcv7 listeria mo	226	32	47.1	428	2	Q74FA3_GEOSL	O5x605 legionella
154	34	50.0	157	2	Q5YT22_NOCFA	Q5yt22 nocardia fa	227	32	47.1	431	2	Q6FBR6_ACIAD	Q74fa3 geobacter s
155	34	50.0	327	2	Q9RLU1_LISMO	Q9rlu1 listeria mo	228	32	47.1	432	2	O88MW0_PSEPK	Q6fbr6 acinetobact
156	34	50.0	327	2	Q8Y3P8_LISMO	Q8y3p8 listeria mo	229	32	47.1	433	2	Q9N4Z0_CAEBL	Q88mw0 pseudomonas
157	34	50.0	412	2	Q5I3L7_ECOLI	Q5i3l7 escherichia	230	32	47.1	433	2	O57L47_SALCH	Q9n4z0 caenorhabdi
158	34	50.0	418	2	Q8TJA6_METAC	Q8tja6 methanosarc	231	32	47.1	433	2	O8ZMX1_SALTY	O57l47 salmonella
159	34	50.0	446	2	Q4ZPF6_PSESY	Q4zpf6 pseudomonas	232	32	47.1	433	2	O824U3_SALTI	Q8zmx1 salmonella
160	34	50.0	446	2	Q87XH6_PESBM	Q87xh6 pseudomonas	233	32	47.1	433	2	O5PID4_SALPA	O8z4j3 salmonella
161	34	50.0	473	2	Q78E98_9MURI	Q78e98 rattus sp.	234	32	47.1	434	2	O6IRC8_CAEBR	O5pid4 salmonella
162	34	50.0	479	2	Q7P2H2_FUSNV	Q7p2h2 fusobacteri	235	32	47.1	435	2	Q6FZ90_BAROU	O6irc8 caenorhabdi
163	34	50.0	494	2	Q96Y04_SULTO	Q96y04 sulfolobus	236	32	47.1	436	2	Q4LK17_9BURK	Q6fz90 bartonella
164	34	50.0	504	2	Q7D0J1_AGR75	Q7d0j1 agrobacteri	237	32	47.1	437	2	Q8XTN1_RALSO	Q4lk17 burkholderi
165	34	50.0	510	2	Q5WHS3_BACSK	Q5whs3 bacillus cl	238	32	47.1	437	2	Q9HXP5_PSEAE	Q8xtn1 ralstonia s
166	34	50.0	526	2	Q56UT8_ORYSA	Q56ut8 oryza sativ	239	32	47.1	437	2	O6ZH22_BURMA	Q9hxp5 pseudomonas
167	34	50.0	526	2	Q8H6G9_ORYSA	Q8h6g9 oryza sativ	240	32	47.1	437	2	Q63RT1_BURPS	Q6zh22 burkholderi
168	34	50.0	636	2	Q8R5V8_FUSNN	Q8r5v8 fusobacteri	241	32	47.1	438	2	O886V6_PSESM	Q63rt1 burkholderi
169	34	50.0	648	1	FOXNI_HUMAN	O15353 homo sapien	242	32	47.1	439	2	Q4L119_9BURK	Q886v6 pseudomonas
170	34	50.0	648	1	FOXNI_MOUSE	O61575 mus musculu	243	32	47.1	439	2	O8XVH5_RALSO	Q4l119 burkholderi
171	34	50.0	648	2	P97715_9MURI	P97715 rattus sp.	244	32	47.1	441	2	Q9BRR1_HUMAN	Q8xvh5 ralstonia s
172	34	50.0	648	2	O5SYK1_MOUSE	O5syk1 mus musculu	245	32	47.1	442	2	Q88I36_PSEPK	Q9brr1 homo sapien
173	34	50.0	829	2	Q7V2T1_PROMP	Q7v2t1 prochloroco	246	32	47.1	443	2	Q9LYY1_PSEPU	O88i36 pseudomonas
174	34	50.0	883	2	Q9LDG7_ARATH	Q9ldg7 arabidopsis	247	32	47.1	444	2	Q9XBD4_AMYOR	Q9lyy1 pseudomonas
175	34	50.0	1125	2	O54GH9_DICDI	O54gh9 dictyostei	248	32	47.1	446	1	CITN_SALDU	Q9xbd4 amycolapops
176	34	50.0	2108	2	Q7VEZ3_MYCBO	Q7vez3 mycobacteri	249	32	47.1	446	1	CITN_SALPU	P31603 salmonella
177	34	50.0	2108	2	O53901_MYCTU	O53901 mycobacteri	250	32	47.1	446	1	CITN_SALTI	P0a2g9 salmonella

251	32	47.1	446	1	CITN_SALTY	P0a2f8	salmonella	324	31	45.6	164	2	Q9DW95	RCWMV	Q9dW95	rat cytomeg
252	32	47.1	446	2	Q57TK4_SALCH	Q57ck4	salmonella	325	31	45.6	185	2	Q6LLC2_PPHOR		Q6llc2	photobacter
253	32	47.1	446	2	Q5PKI7_SALPA	Q5pkI7	salmonella	326	31	45.6	197	2	Q5LOQ5_SILPO		Q5lQ55	silicibacte
254	32	47.1	447	2	Q6WSC1_PSEFL	Q6wsc1	pseudomonas	327	31	45.6	203	2	Q580E7_YTRYP		Q580E7	trypanosoma
255	32	47.1	449	2	Q6XUN5_PSESD	Q6xun5	pseudomonas	328	31	45.6	250	2	Q7URU9_RHOBA		Q7urU9	rhodopirell
256	32	47.1	453	2	Q8XJA0_CLOPE	Q8xja0	clostridium	329	31	45.6	260	2	Q4KG07_PSEF5		Q4KG07	pseudomonas
257	32	47.1	456	2	Q4ZW23_PSESY	Q4zw23	pseudomonas	330	31	45.6	260	2	Q9I3L1_PSEAE		Q9i3L1	pseudomonas
258	32	47.1	457	2	Q6LRW7_CABER	Q6lrw7	caenorhabdi	331	31	45.6	260	2	Q4LRQ1_9BURK		Q4lRQ1	brakholderi
259	32	47.1	458	2	Q16700_CABEL	Q16700	caenorhabdi	332	31	45.6	269	2	Q89JUR0_BRUJA		Q89JUR0	bradyrhizob
260	32	47.1	459	2	Q9HIP6_THEAC	Q9hip6	thermoplasm	333	31	45.6	274	2	Q859B1_9CAUD		Q859B1	bacterioph
261	32	47.1	461	2	Q8L3C1_SERMA	Q8l3c1	serratia ma	334	31	45.6	286	2	Q8YJ90_BRUME		Q8yJ90	bruceella me
262	32	47.1	463	2	Q9HWG1_PSEAE	Q9hwg1	pseudomonas	335	31	45.6	298	2	Q8JW06_YBROM		Q8jW06	spring beau
263	32	47.1	464	2	Q9H9P8_HUMAN	Q9h9p8	homo sapien	336	31	45.6	301	2	Q8RI87_STRCO		Q8ri87	strepptomyc
264	32	47.1	464	2	Q68YB0_RHOSR	Q68yb0	rhodococcus	337	31	45.6	319	2	Q9V497_HALMA		Q9v497	haloarcula
265	32	47.1	464	2	Q6REL7_9NOCA	Q6rel7	rhodococcus	338	31	45.6	352	2	ISPG_GEOSL		Q74d60	geobacter s
266	32	47.1	464	2	Q5YUE1_NOCFA	Q5yue1	nocardia fa	339	31	45.6	353	1	Q4SADI_TETNG		Q4sad1	tetraodon n
267	32	47.1	464	2	Q9IYP0_MOUSE	Q9iyp0	mus musculu	340	31	45.6	356	2	Q4IIV8_GIBZE		Q4iIv8	gibberella
268	32	47.1	467	2	Q8VUZ0_9BRAD	Q8vuz0	bradyrhizob	341	31	45.6	367	2	Q8UJL7_AGR75		Q8uJl7	agrobacteri
269	32	47.1	467	2	Q73LY1_TREDE	Q73ly1	treponema d	342	31	45.6	369	2	Q6IXK9_CABER		Q6ixK9	caenorhabdi
270	32	47.1	467	2	Q5P152_AZOSE	Q5p152	azocarcus sp	343	31	45.6	377	2	Q8PYZ5_METWA		Q8pyZ5	methanosarc
271	32	47.1	470	2	Q8C0S0_MOUSE	Q8c0s0	mus musculu	344	31	45.6	381	2	Q8TJA7_METAC		Q8tJa7	methanosarc
272	32	47.1	488	2	Q97VU3_SULSO	Q97vu3	sulfolobus	345	31	45.6	386	2	Q8PYZ5_METWA		Q8pyZ5	methanosarc
273	32	47.1	492	2	Q4U455_POLCB	Q4u455	polyangium	346	31	45.6	387	2	Q9HMR5_HALSA		Q9hmr5	halobacteri
274	32	47.1	493	2	Q4KHR2_PSEF5	Q4khr2	pseudomonas	347	31	45.6	387	2	Q98MV7_RHILO		Q98mv7	rhizobium l
275	32	47.1	509	1	ZKRI_CHICK	P30373	gallus gall	348	31	45.6	391	2	Q4SFF5_TETNG		Q4sfF5	tetraodon n
276	32	47.1	510	2	Q4SCN6_TETNG	Q4scn6	tetraodon n	349	31	45.6	392	2	Q95YD6_CABEL		Q95yD6	caenorhabdi
277	32	47.1	512	2	Q53K43_ORYSA	Q53k43	oryza sativ	350	31	45.6	394	2	Q60BA8_METCA		Q60ba8	methylococc
278	32	47.1	514	1	TBLIR_HUMAN	Q9bzK7	homo sapien	351	31	45.6	398	2	Q5KUB8_GEOXA		Q5kub8	geobacillus
279	32	47.1	514	1	TBLIR_MOUSE	Q8bhj5	mus musculu	352	31	45.6	400	1	YCEI_BACSV		Q34691	bacillus su
280	32	47.1	519	2	Q9SD16_ARATH	Q9sd16	arabidopsis	353	31	45.6	403	2	Q65W62_MANSM		Q65w62	mannheimia
281	32	47.1	519	2	Q7SZM9_XENLA	Q7szm9	xenopus lae	354	31	45.6	405	2	Q9CM19_PASMU		Q9cm19	pasteurella
282	32	47.1	522	2	Q6GPC6_XENLA	Q6gpc6	xenopus lae	355	31	45.6	405	2	Q8ENE2_OCEIH		Q8ene2	oceanobacil
283	32	47.1	524	2	Q8S220_ORYSA	Q8s220	oryza sativ	356	31	45.6	407	1	Y1I04_HABIN		P71369	haemophilus
284	32	47.1	529	2	Q84WU7_ARATH	Q84wu7	arabidopsis	357	31	45.6	408	2	Q57B25_BRUAB		Q57b25	bruceella ab
285	32	47.1	541	2	Q6NVI6_BRARE	Q6nvi6	brachydanio	358	31	45.6	411	1	AATC_CHICK		P00504	gallus gall
286	32	47.1	552	2	Q62MH3_BURPS	Q62mh3	burkholderi	359	31	45.6	415	2	Q8DX01_STRAS		Q4luy3	burkholderi
287	32	47.1	556	2	Q63WW8_BURPS	Q63ww8	burkholderi	360	31	45.6	415	2	Q8DXX1_STRAS		Q8dx01	streptococc
288	32	47.1	558	2	Q7WKN2_BORBR	Q7wkn2	bordetella	361	31	45.6	415	2	Q8E2V1_STRAS		Q8e2v1	streptococc
289	32	47.1	558	2	Q7W796_BORPA	Q7w796	bordetella	362	31	45.6	417	2	Q8TY81_METKA		Q8ty81	methanopyru
290	32	47.1	558	2	Q7VVT8_BORPE	Q7vvt8	bordetella	363	31	45.6	418	2	Q8XRN4_RALSO		Q8xrn4	raistonia s
291	32	47.1	562	2	Q84PV5_ORYSA	Q84pv5	oryza sativ	364	31	45.6	419	2	Q9VDV8_DROME		Q9vdv8	drosofophila
292	32	47.1	565	2	Q5TZ30_BRARE	Q5tz30	brachydanio	365	31	45.6	426	2	Q4J7U1_SULAC		Q4j7u1	sulfolobus
293	32	47.1	565	2	Q7ZTC0_BRARE	Q7ztc0	brachydanio	366	31	45.6	426	2	Q4LOF8_9BURK		Q4lOf8	burkholderi
294	32	47.1	566	1	YCD6_YEAST	P25370	saccharomyc	367	31	45.6	428	2	Q4ZRQ6_PSESY		Q4zrq6	pseudomonas
295	32	47.1	570	2	Q7NY54_CHRYO	Q7ny54	chromobacte	368	31	45.6	429	2	Q52000_PSEPU		Q52000	pseudomonas
296	32	47.1	579	2	Q7UX97_RHOBA	Q7ux97	rhodopirell	369	31	45.6	429	2	Q9WWZ2_PSEPU		Q9wwZ2	pseudomonas
297	32	47.1	580	2	Q4SP82_TETNG	Q4sp82	tetraodon n	370	31	45.6	429	2	Q88N38_PSEPK		Q88n38	pseudomonas
298	32	47.1	625	2	Q8BZ82_MOUSE	Q8bz82	mus musculu	371	31	45.6	430	2	Q57SC8_SALCH		Q57sc8	salmonella
299	32	47.1	625	2	Q5FWX9_MOUSE	Q5fwx9	mus musculu	372	31	45.6	431	2	Q6R8B5_SODGL		Q6r8b5	sodalis glo
300	32	47.1	663	2	Q5BAD7_EMENT	Q5bad7	aspergillus	373	31	45.6	432	2	Q916Q9_PSEAB		Q916q9	pseudomonas
301	32	47.1	689	2	Q5EC47_RAT	Q5ec47	rattus norv	374	31	45.6	433	2	Q4ZP82_PSESY		Q4zp82	pseudomonas
302	32	47.1	742	2	Q5LFO3_BACFN	Q5lfq3	bacteroides	375	31	45.6	433	2	Q5YUM8_NOCFA		Q5yum8	nocardia fa
303	32	47.1	742	2	Q64WN8_BACFR	Q64wn8	bacteroides	376	31	45.6	433	2	Q87X82_PSESM		Q87x82	pseudomonas
304	32	47.1	796	2	Q4IBG6_GIBZE	Q4ibg6	gibberella	377	31	45.6	435	2	Q7NZC9_CHRVO		Q7nzc9	chromobacte
305	32	47.1	796	2	Q6CNT2_KLULA	Q6cnt2	kluveromyc	378	31	45.6	437	2	Q7M899_WOLSU		Q7m899	wolinella s
306	32	47.1	1180	2	Q7SHH6_NEUCR	Q7shh6	neurospora	379	31	45.6	439	2	Q62AY1_BURMA		Q62ay1	burkholderi
307	32	47.1	1724	2	Q9N583_CABEL	Q9n583	caenorhabdi	380	31	45.6	439	2	Q63K08_BURPS		Q63k08	burkholderi
308	32	47.1	1758	2	Q95Y84_CABEL	Q95y84	caenorhabdi	381	31	45.6	440	2	Q8S7W1_ORYSA		Q8s7w1	oryza sativ
309	32	47.1	1871	2	Q9Z5K6_MYCLE	Q9z5k6	mycobacteri	382	31	45.6	440	2	Q6TMA4_9NOCA		Q6tma4	rhodococcus
310	31.5	46.3	315	2	Q8H9W4_9CAUD	Q8h9w4	pseudomonas	383	31	45.6	441	2	Q5YR16_NOCFA		Q5yr16	nocardia fa
311	31.5	46.3	315	2	Q9F696_BARBA	Q9f696	bartonella	384	31	45.6	443	2	Q4FL43_9RICK		Q4fl43	candidatus
312	31.5	46.3	737	2	Q4SZD1_TETNG	Q4szd1	tetraodon n	385	31	45.6	449	2	Q8ZRC8_SALTY		Q8zrc8	salmonella
313	31	45.6	56	2	Q54UJ21_DICDI	Q54uj21	dictyosteli	386	31	45.6	450	2	Q92YS3_RHIME		Q92ys3	rhizobium m
314	31	45.6	69	2	Q13044_SCYCA	Q13044	scylliorhinu	387	31	45.6	454	1	YAJR_ECOLI		P77726	escherichia
315	31	45.6	83	2	Q6TGR3_PYTMO	Q6tgr3	pythion molu	388	31	45.6	454	2	Q5PEQ3_SALPA		Q5pfq3	salmonella
316	31	45.6	85	2	Q67VG7_ORYSA	Q67vg7	oryza sativ	389	31	45.6	454	2	Q8ZAY2_YERPE		Q8zay2	yersinia pe
317	31	45.6	108	2	Q4FRR6_9GAMM	Q4fir6	psychrobact	390	31	45.6	454	2	Q8Z8W1_SALTI		Q8z8w1	salmonella
318	31	45.6	112	2	Q4RRD3_TETNG	Q4rrd3	tetraodon n	391	31	45.6	454	2	Q665D8_YERPS		Q665d8	yersinia ps
319	31	45.6	132	2	Q01642_DROGR	Q01642	drosofophila	392	31	45.6	454	2	Q6D837_ERWCT		Q6d837	erwinia car
320	31	45.6	142	2	Q8GVX8_ORYSA	Q8gvx8	oryza sativ	393	31	45.6	456	2	Q8ZC53_YERPE		Q8zc53	yersinia pe
321	31	45.6	144	2	Q5BZ05_SCHJA	Q5bz05	schistosoma	394	31	45.6	456	2	Q66DU6_YERPS		Q66du6	yersinia ps
322	31	45.6	158	2	Q74DH7_GEOSL	Q74dh7	geobacter s	395	31	45.6	456	2	Q8XE71_ECO57		Q8xe71	escherichia
323	31	45.6	164	2	Q93CZ0_LACSK	Q93cz0	lactobacill	396	31	45.6	458	2	Q4ZUF0_PSESY		Q4zufe0	pseudomonas

397	31	45.6	458	2	Q83EP3_COXBU	Q83ep3	coxiella bu	470	31	45.6	2073	2	Q73YT8_MYCPA	Q73yt8	mycobacteri
398	31	45.6	460	2	P70737_ALCEU	P70737	alcaligenes	471	31	45.6	2085	2	Q7U0G2_MYCBO	Q7u0g2	mycobacteri
399	31	45.6	462	2	Q7PC06_RICSI	Q7pc06	rickettsia	472	31	45.6	2101	2	Q8VK52_MYCTU	Q8vk52	mycobacteri
400	31	45.6	462	2	Q5LGJ8_BACFN	Q5lgj8	bacteroides	473	31	45.6	2138	2	Q8N6C0_HUMAN	Q8n6c0	mycobacteri
401	31	45.6	462	2	Q89ZJ8_BACTN	Q89zj8	bacteroides	474	31	45.6	2144	2	Q4VM19_HUMAN	Q4vm19	homo sapien
402	31	45.6	462	2	Q92HW3_RICCN	Q92hw3	rickettsia	475	31	45.6	2157	2	Q4VM18_HUMAN	Q4vm18	homo sapien
403	31	45.6	462	2	Q64XE1_BACFR	Q64xe1	bacteroides	476	31	45.6	2179	2	Q4VM17_HUMAN	Q4vm17	homo sapien
404	31	45.6	463	2	Q6OHP7_ALCDE	Q6ohp7	alcaligenes	477	31	45.6	2221	1	CACIC1_HUMAN	CACIC1	homo sapien
405	31	45.6	463	2	Q9RHQ1_VARPD	Q9rhq1	variovorax	478	30.5	44.9	292	2	QANX98_9DELT	QANX98	anaeromyxob
406	31	45.6	463	2	Q8KN29_COMAC	Q8kn29	comamonas a	479	30.5	44.9	389	2	Q6AJ05_DESPS	Q6aj05	desulfocale
407	31	45.6	463	2	Q93LI3_BURCE	Q93li3	burkholderi	480	30	44.1	41	2	Q7QWU5_GIALA	Q7qwU5	giardia lam
408	31	45.6	464	2	Q4ZMS3_PSESY	Q4zms3	pseudomonas	481	30	44.1	89	2	Q73L38_TREDE	Q73l38	treponema d
409	31	45.6	464	2	Q4K562_PSEFS	Q4k562	pseudomonas	482	30	44.1	94	2	Q8BN69_MOUSE	Q8bn69	mus musculu
410	31	45.6	464	2	Q88QK6_PSEPK	Q88qk6	pseudomonas	483	30	44.1	94	2	Q9NHJ5_PLAFA	Q9nhj5	plasmodium
411	31	45.6	464	2	Q5HRH0_STABEQ	Q5hrh0	staphylococ	484	30	44.1	113	2	Q9NHJ5_PLAFA	P52148	escherichia
412	31	45.6	464	2	Q889U2_PSESM	Q889u2	pseudomonas	485	30	44.1	120	2	Q79SA7_9ZZZZ	Q79sa7	incn plasmi
413	31	45.6	466	2	Q4V5J2_DROME	Q4v5j2	drosophila	486	30	44.1	125	2	Q7R6N9_GPOAL	Q7r6n9	giardia lam
414	31	45.6	468	1	LEU2_HAEIN	P44968	haemophilus	487	30	44.1	126	2	Q7R6N9_GIALA	Q7r6n9	giardia lam
415	31	45.6	469	2	Q4QLG2_HAEI8	Q4qlg2	haemophilus	488	30	44.1	137	2	Q9I3Z1_PSEAB	Q9i3z1	pseudomonas
416	31	45.6	469	2	Q65V07_MANSM	Q65v07	mannheimia	489	30	44.1	142	2	Q13032_BRARE	Q13032	brachydanio
417	31	45.6	474	2	Q9HK33_THEAC	Q9hk33	thermoplasma	490	30	44.1	145	2	Q4ZX16_PSESY	Q4zx16	pseudomonas
418	31	45.6	479	2	Q649M0_9ARCH	Q649m0	uncultured	491	30	44.1	146	2	Q65D89_BACLD	Q65d89	bacillus li
419	31	45.6	479	2	Q64A50_9ARCH	Q64a50	uncultured	492	30	44.1	154	2	Q62NR5_BACLD	Q62nr5	bacillus li
420	31	45.6	479	2	Q64ED3_9ARCH	Q64ed3	uncultured	493	30	44.1	155	2	Q755Z1_ASHGO	Q755z1	ashbya gos
421	31	45.6	480	2	Q978M4_THEVO	Q978m4	thermoplasma	494	30	44.1	172	2	Q9Y963_AERPE	Q9y963	aeropyrum p
422	31	45.6	482	2	Q94305_CABEL	Q94305	caenorhabdi	495	30	44.1	173	2	Q6IWI8_SALPU	Q6iwi8	salmonella
423	31	45.6	486	2	Q9HLK4_THEAC	Q9hlk4	thermoplasma	496	30	44.1	178	2	Q5T8X2_HUMAN	Q5t8x2	homo sapien
424	31	45.6	488	2	Q5LYE9_STRT1	Q5lye9	streptococc	497	30	44.1	188	2	Q5H782_STRAT	Q5h782	streptomyce
425	31	45.6	488	2	Q5M312_STRT2	Q5m312	streptococc	498	30	44.1	195	2	Q4PL94_ARATH	Q4pl94	arabidopsis
426	31	45.6	495	2	Q8Z0D2_ANASP	Q8z0d2	anabaena sp	499	30	44.1	214	2	Q58FY5_ARATH	Q58fy5	arabidopsis
427	31	45.6	498	2	Q4Y895_PLACH	Q4y895	plasmodium	500	30	44.1	214	2	Q84RKO_ARATH	Q84rko	arabidopsis
428	31	45.6	503	2	Q6A679_PROAC	Q6a679	propionibac	501	30	44.1	215	1	X315_TREPA	X315	treponema p
429	31	45.6	505	2	Q6IL87_DROME	Q6il87	drosophila	502	30	44.1	220	2	Q8QLX0_9INFA	Q8qlx0	influenza a
430	31	45.6	511	2	Q529L9_MAGGR	Q529l9	magnaporthe	503	30	44.1	222	2	Q6J1T5_9VIRU	Q6j1t5	bacterioph
431	31	45.6	512	2	Q7RJQ3_PLAYO	Q7rjq3	plasmodium	504	30	44.1	222	2	Q72WN7_DESVH	Q72wn7	desulfovibr
432	31	45.6	518	2	Q4IWN9_AZOV1	Q4iwn9	azotobacter	505	30	44.1	235	2	Q840V2_SPHBL	Q840v2	sphingomona
433	31	45.6	520	2	Q8FKB4_ECOL6	Q8fkb4	escherichia	506	30	44.1	239	2	Q75GD0_ORYSA	Q75gd0	oryza sativ
434	31	45.6	521	2	Q8XIF6_GJOIN	Q8xif6	glomus intr	507	30	44.1	239	2	Q8QLW8_9INFA	Q8qlw8	influenza a
435	31	45.6	522	1	TBLIY_HUMAN	Q9bq87	homo sapien	508	30	44.1	246	2	Q4WM25_ASPFU	Q4wm25	aspergillus
436	31	45.6	526	1	TBLIX_HUMAN	Q60907	homo sapien	509	30	44.1	249	2	Q59W69_CANAL	Q59w69	candida alb
437	31	45.6	527	1	TBLX_MOUSE	Q9qxe7	mus musculu	510	30	44.1	251	1	SESA_PROM	SESA	prom
438	31	45.6	527	2	Q84VI6_HORVD	Q84vi6	hordeum vul	511	30	44.1	252	1	WMT1_IAFPR	WMT1	iafpr
439	31	45.6	532	2	Q9S735_ARATH	Q9s735	arabidopsis	512	30	44.1	252	2	Q6EA06_9INFA	Q6ea06	influenza a
440	31	45.6	532	2	Q89SV9_BRAJA	Q89sv9	bradyrhizob	513	30	44.1	252	2	Q77MI3_9INFA	Q77mi3	influenza a
441	31	45.6	534	2	Q7NYH5_CHRVO	Q7nyh5	chromobacte	514	30	44.1	252	2	Q7TGW6_9INFA	Q7tgw6	influenza a
442	31	45.6	538	2	Q9VDV7_DROME	Q9vdv7	drosophila	515	30	44.1	252	2	Q7TGU7_9INFA	Q7tgu7	influenza a
443	31	45.6	540	2	Q59F53_HUMAN	Q59f53	homo sapien	516	30	44.1	252	2	Q80V74_9INFA	Q80v74	influenza a
444	31	45.6	544	2	Q4SOE6_TETNG	Q4soe6	tetraodon n	517	30	44.1	252	2	Q80V75_9INFA	Q80v75	influenza a
445	31	45.6	549	2	Q8H6G6_ORYSA	Q8h6g6	oryza sativ	518	30	44.1	252	2	Q80V77_9INFA	Q80v77	influenza a
446	31	45.6	552	2	Q69T94_ORYSA	Q69t94	oryza sativ	519	30	44.1	252	2	Q80V78_9INFA	Q80v78	influenza a
447	31	45.6	562	2	Q8ZUB1_PYRAE	Q8zub1	pyrobaculum	520	30	44.1	252	2	Q809Y3_9INFA	Q809y3	influenza a
448	31	45.6	563	2	Q4S705_TETNG	Q4s705	tetraodon n	521	30	44.1	252	2	Q809Y5_9INFA	Q809y5	influenza a
449	31	45.6	566	2	Q4W9V3_ASPFU	Q4w9v3	aspergillus	522	30	44.1	252	2	Q809Y9_9INFA	Q809y9	influenza a
450	31	45.6	568	2	Q8I4W7_PLAF7	Q8i4w7	plasmodium	523	30	44.1	252	2	Q809Z5_9INFA	Q809z5	influenza a
451	31	45.6	569	2	Q4R8H1_MACFA	Q4r8h1	macaca fasc	524	30	44.1	252	2	Q809Z7_9INFA	Q809z7	influenza a
452	31	45.6	582	2	Q8H6G7_ORYSA	Q8h6g7	oryza sativ	525	30	44.1	252	2	Q80A03_9INFA	Q80a03	influenza a
453	31	45.6	584	2	Q4FUY0_9GAMM	Q4fuy0	psychrobact	526	30	44.1	252	2	Q80A04_9INFA	Q80a04	influenza a
454	31	45.6	695	2	Q63PL9_BURPS	Q63pl9	burkholderi	527	30	44.1	252	2	Q80A07_9INFA	Q80a07	influenza a
455	31	45.6	700	2	Q62FM2_BURMA	Q62fm2	burkholderi	528	30	44.1	252	2	Q80A07_9INFA	Q80a07	influenza a
456	31	45.6	720	2	Q54S01_DICDI	Q54sq1	dictyosteli	529	30	44.1	252	2	Q80A07_9INFA	Q80a07	influenza a
457	31	45.6	722	1	PALY_CITLI	Q42667	citrus limo	530	30	44.1	252	2	Q80FU1_9INFA	Q80fu1	influenza a
458	31	45.6	725	2	Q54RAS_DICDI	Q54ras	dictyosteli	531	30	44.1	252	2	Q80FU3_9INFA	Q80fu3	influenza a
459	31	45.6	744	2	Q5BET2_EWENI	Q5bet2	aspergillus	532	30	44.1	252	2	Q80FU5_9INFA	Q80fu5	influenza a
460	31	45.6	782	2	Q5IYAI_MAGGR	Q5iyai	magnaporthe	533	30	44.1	252	2	Q80FU7_9INFA	Q80fu7	influenza a
461	31	45.6	805	2	Q4R7B6_MACFA	Q4r7b6	macaca fasc	534	30	44.1	252	2	Q80FU9_9INFA	Q80fu9	influenza a
462	31	45.6	825	2	Q8A2K5_BACTN	Q8a2k5	bacteroides	535	30	44.1	252	2	Q80FV3_9INFA	Q80fv3	influenza a
463	31	45.6	839	2	Q606V3_METCA	Q606v3	methylococc	536	30	44.1	252	2	Q80FV5_9INFA	Q80fv5	influenza a
464	31	45.6	872	2	Q8YT77_ANASP	Q8ytc7	anabaena sp	537	30	44.1	252	2	Q80FW1_9INFA	Q80fw1	influenza a
465	31	45.6	1184	2	Q6BQ08_DEBHA	Q6bq08	debaryomyce	538	30	44.1	252	2	Q80FW3_9INFA	Q80fw3	influenza a
466	31	45.6	1219	2	Q4P4I8_USTMA	Q4p4i8	ustilago ma	539	30	44.1	252	2	Q80FW5_9INFA	Q80fw5	influenza a
467	31	45.6	1582	2	O50437_MYCTU	O50437	mycobacteri	540	30	44.1	252	2	Q80FW7_9INFA	Q80fw7	influenza a
468	31	45.6	1890	2	O49528_ARATH	O49528	arabidopsis	541	30	44.1	252	2	Q80FX1_9INFA	Q80fx1	influenza a
469	31	45.6	2028	2	Q5XPK0_ARATH	Q5xpk0	arabidopsis	542	30	44.1	252	2	Q80FX1_9INFA	Q80fx1	influenza a

543	30	44.1	252	2	Q80FX3_9INFA	Q80fx3 influenza a	616	30	44.1	384	2	Q54QN7_DICDI	Q54qn7 dictyosteli
544	30	44.1	252	2	Q80FX5_9INFA	Q80fx5 influenza a	617	30	44.1	384	2	Q4NRC7_9DELT	Q4nrc7 anaeromyxob
545	30	44.1	252	2	Q80FX7_9INFA	Q80fx7 influenza a	618	30	44.1	384	2	Q501Q0_XENLA	Q501q0 xenopus lae
546	30	44.1	252	2	Q80FX9_9INFA	Q80fx9 influenza a	619	30	44.1	393	2	Q9M562_ORYSA	Q9m562 oryza sativ
547	30	44.1	252	2	Q80FY1_9INFA	Q80fy1 influenza a	620	30	44.1	395	2	Q4J9C7_SULAC	Q4j9c7 sulfolobus
548	30	44.1	252	2	Q80FY3_9INFA	Q80fy3 influenza a	621	30	44.1	398	1	Y1317_METJA	Y58713 methanococc
549	30	44.1	252	2	Q80FY7_9INFA	Q80fy7 influenza a	622	30	44.1	398	2	Q6H167_BACHK	Q6h167 bacillus th
550	30	44.1	252	2	Q80FZ1_9INFA	Q80fz1 influenza a	623	30	44.1	399	2	Q9ZFP5_SALTY	Q9zfp5 salmonella
551	30	44.1	252	2	Q80FZ3_9INFA	Q80fz3 influenza a	624	30	44.1	399	2	Q4MLT2_BACCE	Q4mlt2 bacillus ce
552	30	44.1	252	2	Q80FZ5_9INFA	Q80fz5 influenza a	625	30	44.1	399	2	Q72X31_BACCI	Q72x31 bacillus ce
553	30	44.1	252	2	Q80FZ7_9INFA	Q80fz7 influenza a	626	30	44.1	399	2	Q814L1_BACCR	Q814l1 bacillus ce
554	30	44.1	252	2	Q80FZ9_9INFA	Q80fz9 influenza a	627	30	44.1	399	2	Q81JN5_BACAN	Q81jn5 bacillus an
555	30	44.1	252	2	Q80G01_9INFA	Q80g01 influenza a	628	30	44.1	399	2	Q6HAL8_BACHK	Q6hal8 bacillus th
556	30	44.1	252	2	Q80G03_9INFA	Q80g03 influenza a	629	30	44.1	399	2	Q92MI8_RHIME	Q92mi8 rhizobium m
557	30	44.1	252	2	Q80G05_9INFA	Q80g05 influenza a	630	30	44.1	399	2	Q630I3_BACCZ	Q630i3 bacillus ce
558	30	44.1	252	2	Q80G07_9INFA	Q80g07 influenza a	631	30	44.1	400	2	Q63BE3_BACCZ	Q63be3 bacillus ce
559	30	44.1	252	2	Q80G09_9INFA	Q80g09 influenza a	632	30	44.1	400	2	Q6RGG1_BACLD	Q6rgg1 escherichia
560	30	44.1	252	2	Q80G11_9INFA	Q80g11 influenza a	633	30	44.1	404	2	Q6RGG2_ECOLI	Q6rgg2 escherichia
561	30	44.1	252	2	Q80G13_9INFA	Q80g13 influenza a	634	30	44.1	404	2	Q7B0V2_SALTY	Q7b0v2 salmonella
562	30	44.1	252	2	Q80LX2_9INFA	Q8qlx2 influenza a	635	30	44.1	404	2	Q7BL41_SALET	Q7bl41 salmonella
563	30	44.1	252	2	Q91GM3_9INFA	Q91gm3 influenza a	636	30	44.1	404	2	Q8GJ08_ECOLI	Q8gj08 escherichia
564	30	44.1	252	2	Q91GM8_9INFA	Q91gm8 influenza a	637	30	44.1	404	2	Q8VW40_KLEPN	Q8vw40 klebsiella
565	30	44.1	252	2	Q91GN4_9INFA	Q91gn4 influenza a	638	30	44.1	404	2	Q8VW40_KLEPN	Q8vwn0 vibrio chol
566	30	44.1	252	2	Q9PZF0_9INFA	Q9pzf0 influenza a	639	30	44.1	404	2	Q5PXN3_VIBCH	Q5pxn3 vibrio chol
567	30	44.1	252	2	Q9Q0N5_9INFA	Q9q0n5 influenza a	640	30	44.1	404	2	Q9F0D9_ECOLI	Q9f0d9 escherichia
568	30	44.1	252	2	Q9W834_9INFA	Q9w834 influenza a	641	30	44.1	404	2	Q9F8W2_ECOLI	Q9f8w2 escherichia
569	30	44.1	252	2	Q9WBY8_9INFA	Q9wbz8 influenza a	642	30	44.1	404	2	Q9S6C3_SALTY	Q9s6c3 salmonella
570	30	44.1	252	2	Q9WBZ2_9INFA	Q9wbz2 influenza a	643	30	44.1	404	2	Q9ZH64_SALTY	Q9zh64 salmonella
571	30	44.1	252	2	Q9WBZ4_9INFA	Q9wbz4 influenza a	644	30	44.1	404	2	Q50176_PASMU	Q50i76 pasteurella
572	30	44.1	252	2	Q9WBZ6_9INFA	Q9wbz6 influenza a	645	30	44.1	404	2	Q8VVN0_VIBCH	Q8vvn0 vibrio chol
573	30	44.1	253	2	Q5T8X3_HUMAN	Q5t8x3 homo sapien	646	30	44.1	406	1	FABB_BUCAI	F57193 buchnera ap
574	30	44.1	254	2	Q5LUB1_SILPO	Q5lubl silicibacte	647	30	44.1	408	2	Q5TQD0_ANOGA	Q5tq0 anopheles g
575	30	44.1	254	2	Q5FPE0_GLUOX	Q5fpe0 gluconobact	648	30	44.1	409	2	Q9SJS9_ARATH	Q9sjs9 arabidopsis
576	30	44.1	258	2	Q92TW8_RHIME	Q92tw8 rhizobium m	649	30	44.1	412	2	Q832Z9_ENTFA	Q832z9 enterococcu
577	30	44.1	264	2	Q9UTP5_SCHPO	Q9utp5 schizosacch	650	30	44.1	414	2	Q7U8H8_SYNPX	Q7u8h8 synchococc
578	30	44.1	265	2	Q9M5K0_ORYSA	Q9m5k0 oryza sativ	651	30	44.1	414	2	Q92U74_RHIME	Q92u74 rhizobium m
579	30	44.1	270	1	Y619_TREPA	Q83628 treponema p	652	30	44.1	417	1	TNR25_HUMAN	Q93038 h tumor nec
580	30	44.1	276	2	Q4PL95_ARATH	Q4pl95 arabidopsis	653	30	44.1	417	2	Q5T8X6_HUMAN	Q5t8x6 homo sapien
581	30	44.1	277	2	Q5T8X4_HUMAN	Q5t8x4 homo sapien	654	30	44.1	417	2	Q8LFA5_ARATH	Q8lfa5 arabidopsis
582	30	44.1	284	2	Q8W0R5_SORBI	Q8w0r5 sorghum bic	655	30	44.1	418	2	Q976U9_SULTO	Q976u9 sulfolobus
583	30	44.1	291	2	Q5CZ14_CRYPV	Q5cz14 cryptospori	656	30	44.1	418	2	Q5T8X7_HUMAN	Q5t8x7 homo sapien
584	30	44.1	291	2	Q5CNF6_CRYHO	Q5cnf6 cryptospori	657	30	44.1	418	2	Q5QLG3_ORYSA	Q5qlg3 oryza sativ
585	30	44.1	292	2	Q9U231_CAEBL	Q9u231 caenorhabdi	658	30	44.1	420	2	Q62B40_BURMA	Q62b40 burkholderi
586	30	44.1	297	2	Q5NR91_ZYWMO	Q5nr91 zymomonas m	659	30	44.1	421	2	Q8RWF9_ARATH	Q8rwf9 arabidopsis
587	30	44.1	304	2	Q8XLA4_CLOPE	Q8xla4 clostridium	660	30	44.1	422	2	Q9L125_STRCO	Q9l125 streptomyce
588	30	44.1	307	2	Q8YMW9_ANASP	Q8ymz9 anabaena sp	661	30	44.1	426	2	Q5T8X5_HUMAN	Q5t8x5 homo sapien
589	30	44.1	310	2	Q8SYU3_DROME	Q8syj3 drosophila	662	30	44.1	427	1	YDFJ_ECOLI	P77228 escherichia
590	30	44.1	310	2	Q5BKW9_BRARE	Q5bkw9 brachydanio	663	30	44.1	427	2	Q7ADX7_ECO57	Q7adx7 escherichia
591	30	44.1	320	2	Q52085_POLPA	Q52085 polysphondy	664	30	44.1	427	2	Q63UC9_BURPS	Q63uc9 burkholderi
592	30	44.1	321	2	Q4FEI7_PLAMG	Q4fei7 placopecten	665	30	44.1	427	2	Q8XB44_ECO57	Q8xb44 escherichia
593	30	44.1	325	2	Q8ZPI9_SALTY	Q8zpi9 salmonella	666	30	44.1	429	2	Q96XE1_SULTO	Q96xe1 sulfolobus
594	30	44.1	328	1	GPM6B_MOUSE	P35803 mus musculu	667	30	44.1	429	2	Q9T023_ARATH	Q9t023 arabidopsis
595	30	44.1	333	2	Q949H8_FESBR	Q949h8 festuca pra	668	30	44.1	431	2	Q5KY33_GEOXA	Q5ky33 geobacillus
596	30	44.1	339	2	Q5BAJ1_EMEMI	Q5baj1 aspergillus	669	30	44.1	431	2	Q6SIV8_BACLD	Q6siv8 bacillus fl
597	30	44.1	349	2	Q6ZN88_HUMAN	Q6zn88 homo sapien	670	30	44.1	433	2	Q83Q87_SHIFL	Q83q87 shigella fl
598	30	44.1	350	2	Q7KPA7_LOCMI	Q7kpa7 locusta mig	671	30	44.1	435	2	Q97CN2_THEVO	Q97cn2 thermoplasm
599	30	44.1	353	1	YKFL_YEAST	P35735 saccharomyc	672	30	44.1	435	2	Q4LNM8_9BURK	Q4lnm8 burkholderi
600	30	44.1	354	1	CADH1_EUCGU	Q42726 eucalyptus	673	30	44.1	436	2	Q4LNU5_9BURK	Q4lnu5 burkholderi
601	30	44.1	355	1	CADH2_EUCBO	P50746 eucalyptus	674	30	44.1	436	2	Q6F8A9_ACTAD	Q6f8a9 acinetobact
602	30	44.1	356	1	CADH3_EUCGU	P31655 eucalyptus	675	30	44.1	436	2	Q92NM2_RHIME	Q92nm2 rhizobium m
603	30	44.1	356	1	CADH_EUCGL	O64969 eucalyptus	676	30	44.1	437	2	Q4K948_PSEPS	Q4k948 pseudomonas
604	30	44.1	356	2	Q9FUN8_9MYRT	O9f902 eucalyptus	677	30	44.1	437	2	Q62HP0_BURMA	Q62hp0 burkholderi
605	30	44.1	357	2	O59902_EMEMI	O59902 emericeila	678	30	44.1	437	2	Q63W18_BURPS	Q63w18 burkholderi
606	30	44.1	358	2	O6GUH8_MAIZE	O6guh8 zea mays (m	679	30	44.1	438	2	Q63NM7_BURPS	Q63nm7 burkholderi
607	30	44.1	359	2	O96558_LOCMI	O96558 locusta mig	680	30	44.1	443	2	Q4J3T2_AZOVI	Q4j3t2 azotobacter
608	30	44.1	366	2	O9SYQ1_ARATH	O9syq1 arabidopsis	681	30	44.1	443	2	Q5TYV0_NOCFA	Q5tyv0 nocardia fa
609	30	44.1	369	2	O525R9_MAGGR	O525r9 magnaporthe	682	30	44.1	444	2	Q63KW1_BURPS	Q63kw1 burkholderi
610	30	44.1	374	2	O53019_PASPI	O53019 pasteurella	683	30	44.1	444	2	Q62C15_BURMA	Q62c15 burkholderi
611	30	44.1	376	2	Q4J874_SULAC	Q4j874 sulfolobus	684	30	44.1	444	2	Q62DQ2_BURMA	Q62dq2 burkholderi
612	30	44.1	376	2	Q4I3M7_GIBZE	Q4i3m7 gibberella	685	30	44.1	444	2	Q63IF0_BURPS	Q63if0 burkholderi
613	30	44.1	379	2	O5YPV6_NOCFA	O5ypv6 nocardia fa	686	30	44.1	445	2	Q96X94_SULTO	Q96x94 sulfolobus
614	30	44.1	383	2	Q7Q8M2_ANOGA	Q7q8m2 anopheles g	687	30	44.1	445	2	Q4ZVU7_PSESY	Q4zvuv7 pseudomonas
615	30	44.1	384	2	Q8ZVE1_PYRAB	Q8zve1 pyrobaculum	688	30	44.1	445	2	Q87YJ5_PSESM	Q87yj5 pseudomonas

689	30	44.1	446	2	Q9HLT4_THEAC	Q9hlt4 thermoplasm
690	30	44.1	446	2	Q584D0_9TRYP	Q584d0 trypanosoma
691	30	44.1	446	2	Q7W5L6_BORPA	Q7w5l6 bordetella
692	30	44.1	446	2	Q7WD52_BORBR	Q7wd52 bordetella
693	30	44.1	449	2	Q89W04_BRATJ	Q89w04 bradyrhizob
694	30	44.1	450	2	Q82MF2_STRAW	Q82mf2 streptomyce
695	30	44.1	452	2	Q82S97_NITEU	Q82s97 nitrosomona
696	30	44.1	454	2	Q8YOF1_RALSO	Q8yof1 ralstonia s
697	30	44.1	455	2	Q8FHC9_ECOL6	Q8fhc9 escherichia
698	30	44.1	457	2	Q7VUM3_BORPE	Q7vum3 bordetella
699	30	44.1	457	2	Q7W1Z2_BORPA	Q7w1z2 bordetella
700	30	44.1	457	2	Q7WQX0_BORBR	Q7wqx0 bordetella
701	30	44.1	458	2	Q7UR88_RHOBA	Q7ur88 rhodopirell
702	30	44.1	459	2	Q5PHH3_SALPA	Q5phh3 salmonella
703	30	44.1	459	2	Q8Z6Z5_SALTI	Q8z6z5 salmonella
704	30	44.1	459	2	Q83DE6_COXBU	Q83de6 coxiella bu
705	30	44.1	463	2	Q4NJH2_9M1CC	Q4njh2 arthrobacte
706	30	44.1	463	2	Q636R1_BACCZ	Q636r1 bacillus ce
707	30	44.1	465	2	Q65XC9_ORYSA	Q65xc9 oryza sativ
708	30	44.1	467	2	Q4LYN1_9BURK	Q4lyn1 burkholderi
709	30	44.1	469	2	Q9HY31_PSEAE	Q9hy31 pseudomonas
710	30	44.1	471	2	Q97U43_SULSO	Q97u43 sulfolobus
711	30	44.1	479	2	Q741S2_IACJO	Q741s2 lactobacill
712	30	44.1	493	2	Q4JAC9_SULAC	Q4jac9 sulfolobus
713	30	44.1	495	2	Q627F2_CAEBR	Q627f2 caenorhabdi
714	30	44.1	495	2	Q6N0U9_RHOBA	Q6n0u9 rhodopseu
715	30	44.1	495	2	Q92UJ3_RHIME	Q92uj3 rhizobium m
716	30	44.1	503	2	Q57PD1_SALCH	Q57pd1 salmonella
717	30	44.1	508	2	Q7NJW4_GJOVI	Q7njw4 gloeobacter
718	30	44.1	509	2	Q84LI0_HORVD	Q84li0 hordeum vul
719	30	44.1	514	2	Q9SLJ9_ARATH	Q9slj9 arabidopsis
720	30	44.1	517	1	FOXN4_HUMAN	Q96nzi homo sapien
721	30	44.1	517	2	Q89XJ0_BRAJA	Q89xj0 bradyrhizob
722	30	44.1	521	2	Q00908_9FUNG	Q00908 glomus vers
723	30	44.1	521	2	Q8H6E0_HORVD	Q8h6e0 hordeum vul
724	30	44.1	525	2	Q7YMD9_WHEAT	Q7ymd9 triticum ae
725	30	44.1	525	2	Q84LH9_HORVD	Q84lh9 hordeum vul
726	30	44.1	525	2	Q84TL8_HORVU	Q84tl8 hordeum vul
727	30	44.1	525	2	Q93WQ8_9POAL	Q93wq8 triticum ae
728	30	44.1	525	2	Q93WQ9_9POAL	Q93wq9 triticum ae
729	30	44.1	525	2	Q93WR0_9POAL	Q93wr0 triticum ae
730	30	44.1	526	2	Q7XDZ7_ORYSA	Q7xdz7 oryza sativ
731	30	44.1	526	2	Q8H6H3_ORYSA	Q8h6h3 oryza sativ
732	30	44.1	527	2	Q56UV2_ORYSA	Q56uv2 oryza sativ
733	30	44.1	527	2	Q8H6H4_ORYSA	Q8h6h4 oryza sativ
734	30	44.1	528	2	Q56UUI_ORYSA	Q56uui oryza sativ
735	30	44.1	528	2	Q8GSD9_ORYSA	Q8gsd9 oryza sativ
736	30	44.1	534	2	Q9EWX5_STRCO	Q9ewx5 streptomyce
737	30	44.1	535	2	Q828X0_STRAW	Q828x0 streptomyce
738	30	44.1	539	2	Q4PDE5_USTMA	Q4pde5 ustilago ma
739	30	44.1	539	2	Q6GUH9_MAYZE	Q6guh9 zea mays (m
740	30	44.1	539	2	Q88RS2_PSEBK	Q88rs2 pseudomonas
741	30	44.1	541	2	Q8H074_ORYSA	Q8h074 oryza sativ
742	30	44.1	541	2	Q8H6G5_ORYSA	Q8h6g5 oryza sativ
743	30	44.1	541	2	Q8H6G8_ORYSA	Q8h6g8 oryza sativ
744	30	44.1	545	2	Q61FBI_CAEBR	Q61fbi caenorhabdi
745	30	44.1	550	2	Q9DG30_BRARE	Q9dg30 brachydanio
746	30	44.1	550	2	Q9PT94_BRARE	Q9pt94 brachydanio
747	30	44.1	556	2	Q9GUG2_9TRYP	Q9gu92 trypanosoma
748	30	44.1	556	2	Q9VFG2_DROME	Q9vf92 drosophila
749	30	44.1	557	2	Q8MT31_DROME	Q8mt31 drosophila
750	30	44.1	557	2	Q9VFG1_DROME	Q9vfg1 drosophila
751	30	44.1	558	2	Q8KLT0_RHISH	Q8klc0 rhizobium s
752	30	44.1	560	2	Q4IMZ4_GIBZE	Q4imz4 gibberella
753	30	44.1	560	2	Q9VFG0_DROME	Q9vf90 drosophila
754	30	44.1	565	2	Q4V514_DROME	Q4v514 drosophila
755	30	44.1	566	2	Q9WZU1_THEMA	Q9wzui thermotoga
756	30	44.1	572	2	Q91TK6_TUHV1	Q91tk6 tupaidi her
757	30	44.1	575	2	Q9BKR9_CAEBL	Q9bkr9 caenorhabdi
758	30	44.1	575	2	Q66KG0_XENLA	Q66kg0 xenopus lae
759	30	44.1	578	2	Q8DCK1_VIBVU	Q8dck1 vibrio vuln
760	30	44.1	578	2	Q7MHA6_VIBVY	Q7mha6 vibrio vuln
761	30	44.1	585	2	Q4V539_DROME	Q4v539 drosophila

835	29.5	43.4	321	2	Q561P6_BRARE	Q561p6 brachydanio	908	29	42.6	336	2	Q4J4G0_AZOVI	Q4j4g0 azotobacter
836	29.5	43.4	917	2	Q89KU0_BRAJA	Q89ku0 bradyrhizob	909	29	42.6	338	2	Q9RL00_STRCO	Q9rl00 streptomyce
837	29.5	43.4	1000	2	Q8JM39_9NUCL	Q8jm39 mamestra co	910	29	42.6	343	2	Q82RC2_STRAW	Q82rc2 streptomyce
838	29.5	43.4	1064	2	Q57V44_9TRYF	Q57v44 trypanosoma	911	29	42.6	344	2	Q87D70_XYLF	Q87d70 xylella fas
839	29	42.6	77	2	Q96481_PLAFA	Q96481 plasmodium	912	29	42.6	344	2	Q9PBZ2_XYLF	Q9pbz2 xylella fas
840	29	42.6	78	2	Q4YA70_PLABE	Q4ya70 plasmodium	913	29	42.6	349	2	Q9RW33_DEIRA	Q9rw33 deinococcus
841	29	42.6	84	2	Q7YRW7_CAPHI	Q7yrw7 capra hircu	914	29	42.6	352	2	Q50170_MYCLE	Q50170 mycobacteri
842	29	42.6	96	2	Q95J81_HORSE	Q95j81 equus cabal	915	29	42.6	354	2	Q6LH52_PHOPR	Q6lh52 photobacter
843	29	42.6	98	2	Q9YR19_HCMV	Q9yr19 human cytom	916	29	42.6	356	2	Q9NF90_LEIMA	Q9nf90 leishmania
844	29	42.6	100	2	Q9YRJ4_HCMV	Q9yrj4 human cytom	917	29	42.6	357	2	Q22066_CAEEL	Q22066 caenorhabdi
845	29	42.6	106	2	Q7VKJ2_BORPE	Q7vkJ2 bordetella	918	29	42.6	358	2	Q57588_FUGRU	Q57588 fugu rubrip
846	29	42.6	106	2	Q7W8X7_BORPA	Q7w8x7 bordetella	919	29	42.6	361	2	Q96M90_HUMAN	Q96m90 homo sapien
847	29	42.6	106	2	Q7WK88_BORBR	Q7wk88 bordetella	920	29	42.6	362	2	Q7U1T5_MYCBO	Q7u1t5 mycobacteri
848	29	42.6	110	2	Q8VJM5_MYCTU	Q8vjm5 mycobacteri	921	29	42.6	362	2	Q06408_MYCTU	Q06408 mycobacteri
849	29	42.6	111	2	Q8ZM12_PYRAE	Q8zm12 pyrobaculum	922	29	42.6	368	2	Q06408_MYCTU	Q06408 mycobacteri
850	29	42.6	113	2	Q4J078_AZOVI	Q4j078 azotobacter	923	29	42.6	368	2	Q72R11_LEPIC	Q72r11 leptospira
851	29	42.6	115	2	Q8PZH1_METMA	Q8pzh1 methanosarc	924	29	42.6	368	2	Q8F489_LEPIN	Q8f489 leptospira
852	29	42.6	115	2	Q95S02_DROME	Q95s02 drosophila	925	29	42.6	368	2	Q9CB88_MYCLE	Q9cb88 mycobacteri
853	29	42.6	127	2	Q76992_TAESA	Q76992 taenia sagi	926	29	42.6	371	2	Q97Z05_SULSO	Q97z05 sulfolobus
854	29	42.6	127	2	Q8RN34_CAMJE	Q8rn34 campylobact	927	29	42.6	372	2	Q4JBP2_SULAC	Q4jbp2 sulfolobus
855	29	42.6	127	2	Q5HSN5_CAMJR	Q5hsn5 campylobact	928	29	42.6	374	2	Q974L5_SULTO	Q974l5 sulfolobus
856	29	42.6	130	1	OSTN_MOUSE	P61364 mus musculu	929	29	42.6	377	2	Q8PYZ6_METMA	Q8pyz6 methanosarc
857	29	42.6	132	1	OSTN_RAT	P61365 rattus norv	930	29	42.6	385	2	Q9NF91_LEIMA	Q9nf91 leishmania
858	29	42.6	133	1	OSTN_HUMAN	P61366 homo sapien	931	29	42.6	386	2	Q8RY43_SEECE	Q8ry43 secale cere
859	29	42.6	137	2	Q97D00_CLOAB	Q97d00 clostridium	932	29	42.6	387	2	Q5CQ92_CRYPV	Q5cq92 cryptospori
860	29	42.6	145	2	Q4N7A8_THEPA	Q4n7a8 theileria p	933	29	42.6	392	2	Q6NNW8_DROME	Q6nnw8 drosophila
861	29	42.6	145	2	Q9JX84_NEIMA	Q9jx84 neisseria m	934	29	42.6	392	2	Q4VDI1_PPOAL	Q4vdi1 juncus trif
862	29	42.6	145	2	Q9K1B7_NEIMB	Q9k1b7 neisseria m	935	29	42.6	392	2	Q4TJH6_9SPHN	Q4tjh6 erythroact
863	29	42.6	150	2	Q6ZVS4_HUMAN	Q6zvs4 homo sapien	936	29	42.6	396	2	Q6LPQ0_PROPR	Q6lpq0 photobacter
864	29	42.6	150	2	Q7MU38_PORGI	Q7mu38 porphyromon	937	29	42.6	398	2	Q5KYE5_GEOXA	Q5kye5 geobacillus
865	29	42.6	152	2	Q8MPC5_TAESO	Q8mpc5 taenia soli	938	29	42.6	399	1	PHHC_PSEAE	P43336 pseudomonas
866	29	42.6	161	2	Q8NAR1_HUMAN	Q8nar1 homo sapien	939	29	42.6	399	2	Q21342_CAEEL	Q21342 caenorhabdi
867	29	42.6	166	2	Q4XUA9_PLACH	Q4xua9 plasmodium	940	29	42.6	403	2	Q746S0_GEOSL	Q746s0 geobacter s
868	29	42.6	169	2	Q9PVQ0_XENLA	Q9pvq0 xenopus lae	941	29	42.6	404	2	Q5T953_HUMAN	Q5t953 homo sapien
869	29	42.6	170	2	Q4YSV7_PLABE	Q4ysv7 plasmodium	942	29	42.6	406	2	Q99J55_MOUSE	Q99j55 mus musculu
870	29	42.6	173	2	Q8FRJ6_COREF	Q8frj6 corynebacte	943	29	42.6	408	2	Q7D7T7_MYCTU	Q7d7t7 mycobacteri
871	29	42.6	191	2	Q7NV46_CHRYO	Q7nv46 chromobacte	944	29	42.6	409	2	Q5B2N7_EMENTI	Q5b2n7 aspergillus
872	29	42.6	192	2	Q00503_9HYPO	Q00503 calonectria	945	29	42.6	409	2	Q5LQD4_SILPO	Q5lqd4 silicibacte
873	29	42.6	192	2	Q4TLE8_9SPHN	Q4tle8 erythroact	946	29	42.6	409	2	Q5PQP0_RAT	Q5pqp0 rattus norv
874	29	42.6	211	2	Q4Z083_PLABE	Q4z083 plasmodium	947	29	42.6	414	2	Q9KMV4_VIBCH	Q9kmv4 vibrio chol
875	29	42.6	215	1	DEOC_LACPL	Q88z64 lactobacill	948	29	42.6	419	1	GLPB_ECOS7	Q8xe13 escherichia
876	29	42.6	215	2	Q67M34_SYMTN	Q67m34 symbiobacte	949	29	42.6	419	1	GLPB_ECOS6	Q8ffn4 escherichia
877	29	42.6	216	2	Q5LRC4_SILPO	Q5lrc4 silicibacte	950	29	42.6	419	1	GLPB_ECOS7	P13033 escherichia
878	29	42.6	217	2	Q01730_BRALA	Q01730 branchiosto	951	29	42.6	419	1	GLPB_SHIFL	Q83m10 shigella fl
879	29	42.6	224	2	Q98NM0_RHIL0	Q98nm0 rhizobium l	952	29	42.6	422	2	Q8ZUI5_PYRAE	Q8zu15 pyrobaculum
880	29	42.6	224	2	Q6TUF5_RAT	Q6tuf5 rattus norv	953	29	42.6	422	2	Q5QW70_ORYSA	Q5qw70 oryza sativ
881	29	42.6	236	2	Q6FX03_CANGA	Q6fx03 candida gla	954	29	42.6	422	2	Q7TZB7_MYCBO	Q7tzb7 mycobacteri
882	29	42.6	237	2	Q6ETZ8_ORYSA	Q6etz8 oryza sativ	955	29	42.6	422	2	Q07730_MYCTU	Q07730 mycobacteri
883	29	42.6	237	2	Q5SUX9_MOUSE	Q5sux9 mus musculu	956	29	42.6	424	2	Q73ZH7_MYCPA	Q73zh7 mycobacteri
884	29	42.6	239	2	Q89M29_BRAJA	Q89m29 bradyrhizob	957	29	42.6	426	2	Q55F21_DICDI	Q55f21 dictyosteli
885	29	42.6	243	2	Q75BA1_ASHGO	Q75ba1 ashbya goss	958	29	42.6	426	2	Q4UVU6_XANCP	Q4uvu6 xanthomonas
886	29	42.6	244	2	Q851B5_ORYSA	Q851b5 oryza sativ	959	29	42.6	426	2	Q8P891_XANCP	Q8p891 xanthomonas
887	29	42.6	252	2	Q6FCJ5_ACTAD	Q6fcj5 acinetobact	960	29	42.6	428	2	Q5NE71_FRATT	Q5ne71 francisella
888	29	42.6	263	2	Q98KE1_RHIL0	Q98ke1 rhizobium l	961	29	42.6	428	2	Q5WXC7_LEGFL	Q5wxc7 legionella
889	29	42.6	264	2	Q8AM09_BRARE	Q8aw09 brachydanio	962	29	42.6	429	1	SYN_CORGL	Q8ng07 corynebacte
890	29	42.6	265	2	Q915Y6_PSEAE	Q915y6 pseudomonas	963	29	42.6	430	2	Q4NLX3_9MICC	Q4nlx3 arthrobacte
891	29	42.6	275	2	Q6D6X8_ERMCT	Q6d6x8 erwinia car	964	29	42.6	431	2	Q54041_PSEAE	Q54041 pseudomonas
892	29	42.6	280	2	Q8SU22_ENCCU	Q8su22 encephalito	965	29	42.6	431	2	Q8CC26_MOUSE	Q8cc26 mus musculu
893	29	42.6	280	2	Q5P1S3_AZOSE	Q5p1s3 azoarcus sp	966	29	42.6	432	2	Q5UXM1_HUMAN	Q5uxm1 homo sapien
894	29	42.6	280	2	Q5YYZ3_NOCFA	Q5yyz3 nocardia fa	967	29	42.6	434	2	Q4LRB1_9BURK	Q4lrb1 burkholderi
895	29	42.6	281	2	Q6M140_METMP	Q6m140 methanococc	968	29	42.6	434	2	Q63TZ2_BURPS	Q63tz2 burkholderi
896	29	42.6	283	2	Q53R38_HUMAN	Q53r38 homo sapien	969	29	42.6	434	2	Q8UDN2_AGRTS	Q8udn2 agrobacteri
897	29	42.6	286	2	Q7ZZ43_BRARE	Q7zz43 brachydanio	970	29	42.6	434	2	Q7TML8_MOUSE	Q7tml8 mus musculu
898	29	42.6	286	2	Q8T4S9_AEDAE	Q8t4s9 aedes aegypt	971	29	42.6	435	2	Q553Q5_DICDI	Q553q5 dictyosteli
899	29	42.6	290	2	Q8T4T0_AEDAE	Q8t4t0 aedes aegypt	972	29	42.6	435	2	Q6G2S7_BARHE	Q6g2s7 bartonella
900	29	42.6	290	2	Q8T4T1_AEDAE	Q8t4t1 aedes aegypt	973	29	42.6	435	2	Q6N7B6_RHOPA	Q6n7b6 rhodopsendo
901	29	42.6	290	2	Q8T4T2_AEDAE	Q8t4t2 aedes aegypt	974	29	42.6	437	2	Q89IV5_BRAJA	Q89iv5 bradyrhizob
902	29	42.6	290	2	Q95P61_AEDAE	Q95p61 aedes aegypt	975	29	42.6	438	1	SHIA_ECOLI	P76350 escherichia
903	29	42.6	290	2	Q9BJM8_AEDAE	Q9bjm8 aedes aegypt	976	29	42.6	438	2	Q7ACT1_ECOS7	Q7act1 escherichia
904	29	42.6	295	2	Q5A4U4_CANAL	Q5a4u4 candida alb	977	29	42.6	438	2	Q65UQ7_MANSM	Q65uq7 mannheimia
905	29	42.6	314	2	Q810T0_MOUSE	Q810t0 mus musculu	978	29	42.6	438	2	Q8X4U5_ECOS7	Q8x4u5 escherichia
906	29	42.6	315	2	Q7UPU5_RHOBA	Q7upu5 rhodopirell	979	29	42.6	438	2	Q8FGD5_ECOS6	Q8fgd5 escherichia
907	29	42.6	329	2	Q75CB3_ASHGO	Q75cb3 ashbya goss	980	29	42.6	438	2		

981	29	42.6	440	1	YHUE_ECOLI	P37643	escherichia
982	29	42.6	440	2	Q57IL3_SALCH	Q57IL3	salmonella
983	29	42.6	440	2	Q5PUR5_SALPA	Q5PUR5	salmonella
984	29	42.6	440	2	Q83PS5_SHIFL	Q83PS5	shigella fl
985	29	42.6	440	2	Q8FCI0_ECOL6	Q8FCI0	escherichia
986	29	42.6	440	2	Q8X4K9_ECO57	Q8X4K9	escherichia
987	29	42.6	440	2	Q8Z282_SALTI	Q8Z282	salmonella
988	29	42.6	440	2	Q8ZLC3_SALTY	Q8ZLC3	salmonella
989	29	42.6	441	2	Q6D950_ERWCT	Q6D950	erwinia car
990	29	42.6	442	2	Q8PJUP6_XANAC	Q8PJUP6	xanthomonas
991	29	42.6	443	2	Q4JVE8_CORJK	Q4JVE8	corynebacte
992	29	42.6	443	2	Q62IU8_BURMA	Q62IU8	burkholderi
993	29	42.6	445	2	Q88K80_PSEBK	Q88K80	pseudomonas
994	29	42.6	446	2	Q4REF0_TETNG	Q4REF0	tetradodon n
995	29	42.6	447	2	Q63SJ3_BURPS	Q63SJ3	burkholderi
996	29	42.6	448	2	Q93TD3_PSEYM	Q93TD3	pseudomonas
997	29	42.6	448	2	Q88BN1_PSESM	Q88BN1	pseudomonas
998	29	42.6	448	2	Q88BT7_PSESM	Q88BT7	pseudomonas
999	29	42.6	449	2	Q45082_BURCE	Q45082	burkholderi
1000	29	42.6	451	1	MURD_GEOXA	Q510X7	geobacillus

ALIGNMENTS

RESULT 1
Q6VYM3_BRARE PRELIMINARY; PRT; 106 AA.

AC Q6VYM3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Atrial natriuretic factor.
GN Name=npa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22959386; PubMed=14573521; DOI=10.1242/dev.00838;
RA Berdugo E., Coleman H., Lee D.H., Strainier D.Y., Yelon D.;
RT "Mutation of weak atrium/atrial myosin heavy chain disrupts atrial
function and influences ventricular morphogenesis in zebrafish.";
RL Development 130:6121-6129(2003).
DR EMBL; AY319419; AAQ87026.1; -; mRNA.
DR ZFIN; ZDB-GENE-030131-95; npa.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 106 AA; 11528 MW; C44A659CD9DFE9CA CRC64;

Query Match 83.8%; Score 57; DB 2; Length 106;
Best Local Similarity 58.8%; Pred. No. 0.00027;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 85 CFGGRIDRIGSSSTLGC 101

RESULT 2
ANF_ACITR STANDARD; PRT; 142 AA.
ID ANF_ACITR
AC P83964;

DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANP) (Prepronatriodilatin).
GN Name=np;
OS Acipenser transmontanus (White sturgeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
OC Acipenser.
OX NCBI_TaxID=7904;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RC TISSUE=Heart atrium;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
key role in cardiovascular homeostasis. Has a cGMP-stimulating
activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in heart atrium and to a lower
extent in heart ventricle, but not in brain.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

DR EMBL; AB087728; BAD02835.1; -; mRNA.
DR InterPro; IPR002407; At_natriurtcpep.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; Ac_natriurtcpep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 111
FT PEPTIDE 113 142 Atrial natriuretic factor.
FT DISULFID 120 136 By similarity.
SQ SEQUENCE 142 AA; 15888 MW; 382B87FB44178CD9 CRC64;

Query Match 83.8%; Score 57; DB 1; Length 142;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 120 CFGSRIDRIGSSSMGC 136

RESULT 3
Q7T217_ONCMY PRT; 146 AA.
ID Q7T217_ONCMY PRELIMINARY;
AC Q7T217;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Atrial natriuretic peptide.
GN Name=anp;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Inoue K., Russel M.J., Olson K.R., Takei Y.,
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB076603; BAC77769.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriurctpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 146 AA; 16043 MW; FED2CE3C79121BD0 CRC64;

Query Match 83.8%; Score 57; DB 2; Length 146;
Best Local Similarity 58.8%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
DB 124 CFGARMDRIGTSSGLGC 140

RESULT 4
O78AW6 SALSA
ID O78AW6_SALSA PRELIMINARY; PRT; 148 AA.
AC O78AW6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Cardiac peptide precursor.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20114377; PubMed=10650955; DOI=10.1210/en.141.2.731;
RA Majalahti-Palvaainen T., Hirvonen M., Tervonen V., Ilves M.,
RA Ruskoaho H., Vuolteenaho O.;
RT "Gene structure of a new cardiac peptide hormone: a model for heart-specific gene expression.";
RL Endocrinology 141:731-740(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Vuolteenaho O.J.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006421; CAA07023.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriurctpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Signal; Vasoactive.
FT SIGNAL 1 119 Potential.
FT CHAIN 120 148 cardiac peptide.
SQ SEQUENCE 148 AA; 16236 MW; 934985642C25C739 CRC64;

Query Match 83.8%; Score 57; DB 2; Length 148;
Best Local Similarity 58.8%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
DB 126 CFGARMDRIGTSSGLGC 142

RESULT 5
O9YGJ1 SALSA
ID O9YGJ1_SALSA PRELIMINARY; PRT; 152 AA.
AC O9YGJ1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cardiac hormone.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tervonen V., Arjamaa O., Ruskoaho H., Vuolteenaho O.;
RT "New vasoactive cardiac hormone released by mechanical load.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Vuolteenaho O.J.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001806; CAA05022.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriurctpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT CHAIN 124 152 cardiac hormone.
SQ SEQUENCE 152 AA; 16740 MW; EID3E38A159CFEEA CRC64;

Query Match 83.8%; Score 57; DB 2; Length 152;
Best Local Similarity 58.8%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
DB 130 CFGARMDRIGTSSGLGC 146

RESULT 6
ANF_RANRI
ID ANF_RANRI STANDARD; PRT; 30 AA.
AC P09196;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Atrial natriuretic factor (ANF) (Atrial natriuretic peptide) (ANP).
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OC Pelophylax.
OX NCBI_TaxID=8406;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Heart atrium;

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RX MEDLINE=89005705; PubMed=2971573; DOI=10.1016/0014-5793(88)80501-5;
RA Lazure C., Ong H., McNicol N., Netchitallo P., Chretien M.,
RA de Lean A., Vaudry H.;
RT "The amino acid sequences of frog heart atrial natriuretic-like
RT peptide and mammalian ANF are closely related.";
RL FEBS Lett. 238:300-306(1988).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; S01657; S01657.
DR InterPro; IPR002407; At_natriuretcpep.
DR InterPro; IPR002408; Br_natriuretcpep.
DR InterPro; IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; At_natriuretcpep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005107; At_natriuretcpep; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Vasoactive.
FT DISULFID 11 27
SQ SEQUENCE 30 AA; 3263 MW; 175A946321C27DA0 CRC64;

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Query Match      82.4%; Score 56; DB 1; Length 30;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 1 CFGXXXXRIGXXSXXGC 17
Db 11 CFGRRMDRIGSMSSLCG 27

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RESULT 7
Q4TD23 TETNG PRELIMINARY; PRT; 83 AA.
AC Q4TD23;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF6568, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00003028001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfaila G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

```

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RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01006568; CAF89209.1; -: Genomic_DNA.
DR InterPro; IPR002408; Br_natriuretcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 83 83
SQ SEQUENCE 83 AA; 9432 MW; 5D020DD1512E2DF6 CRC64;

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Query Match      82.4%; Score 56; DB 2; Length 83;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 1 CFGXXXXRIGXXSXXGC 17
Db 65 CFGRRMDRIGSMSSLCG 81

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RESULT 8
ANF_CAVPO STANDARD; PRT; 128 AA.
ID ANF_CAVPO
AC P27596;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANP) (Prepronatriodilatin) [Contains: Cardiodilatin-related peptide
DE (CDP)] (Fragment).
GN Name=NPPA;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart atrium;
RA Maegert H.-J., Hanke M., Schmeding G., Teuteberg K., Schulz-Knappe P.,
RA Forsmann W.-G.;
RL Submitted (MAR-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: Adult.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X58562; CAA41442.1; -: mRNA.
DR PIR; S14872; S14872.
DR InterPro; IPR002407; At_natriuretcpep.
DR InterPro; IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; At_natriuretcpep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.

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DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005107; Ac_natriurtcep; 1.
DR Prodom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Vasoactive.
FT PEPTIDE 1 30 Cardiolactin-related peptide.
FT PEPTIDE 99 126 Atrial natriuretic factor.
FT DISULFID 105 121 By similarity.
FT NON_TER 1 1
SQ SEQUENCE 128 AA; 13966 MW; EFC5004BADDEF318 CRC64;
Query Match 82.4%; Score 56; DB 1; Length 128;
Best Local Similarity 58.8%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CFGXXXDRIGXXSXXGC 17
Db 105 CFGGRMDRIGAGSLSGC 121
RESULT 9
ANFB_FUGRU STANDARD; PRT; 133 AA.
AC Q805D7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Brain natriuretic peptide precursor (B-type natriuretic peptide).
GN Name=BNP;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB089934; BAC57070.1; -; mRNA.
DR Ensembl; SINFRUG00000135753; Fugu rubripes.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 ?
FT PEPTIDE ? 133 Brain natriuretic peptide.
FT DISULFID 108 124 By similarity.

SQ SEQUENCE 133 AA; 14746 MW; FD4541B255A33436 CRC64;
Query Match 82.4%; Score 56; DB 1; Length 133;
Best Local Similarity 58.8%; Pred. No. 0.00054;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CFGXXXDRIGXXSXXGC 17
Db 108 CFGGRMDRIGSMSSSLGC 124
RESULT 10
ANFB_OREMO STANDARD; PRT; 138 AA.
AC Q805E8;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Brain natriuretic peptide precursor (B-type natriuretic peptide).
GN Name=BNP;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiini;
OC Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB087284; BAC55025.1; -; mRNA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 ?
FT PEPTIDE ? 138 Brain natriuretic peptide.
FT DISULFID 111 127 By similarity.
SQ SEQUENCE 138 AA; 15189 MW; 5A023AB1F4F452FA CRC64;
Query Match 82.4%; Score 56; DB 1; Length 138;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CFGXXXDRIGXXSXXGC 17
Db 111 CFGGRMDRIGSMSSSLGC 127

RESULT 11
Q4T953_TETNG
ID Q4T953_TETNG PRELIMINARY; PRT; 138 AA.
AC Q4T953;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Chromosome undetermined SCAF7638, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00004914001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01007638; CAF90579.1; -; Genomic_DNA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15212 MW; E244D7D6F9BE3BF4 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 138;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
Db 117 CFGARMDRIGNASGLGC 133

RESULT 12
ANF_FUGRU STANDARD; PRT; 139 AA.
AC Q805D8;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANF) (Prepronatriodilatin).
GN Name=ANP;

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----

DR EMBL; AB089933; BAC57069.1; -; mRNA.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; At_natriurtcep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 112
FT PEPTIDE 115 139 Atrial natriuretic factor.
FT DISULFID 118 134 By similarity.
SQ SEQUENCE 139 AA; 15569 MW; EC9BCBE9D5C31220 CRC64;

Query Match 82.4%; Score 56; DB 1; Length 139;
Best Local Similarity 58.8%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
Db 118 CFGARMDRIGNASGLGC 134

RESULT 13
ANF_OREMO STANDARD; PRT; 140 AA.
AC Q805E9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANF) (Prepronatriodilatin).
GN Name=ANP;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilaplini;
OC Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;

```

RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RL sturgeon: identification of BNP in fish lineage.";
RT J. Mol. Endocrinol. 32:547-555(2004).
CC -1- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB087283; BAC55024.1; -; mRNA.
CC InterPro; IPR002407; At_natriurtcep.
CC InterPro; IPR000663; Natr_peptide.
CC PANTHER; PTHR11415; At_natriurtcep; 1.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00711; ANATPEPTIDE.
CC PRINTS; PR00710; NATPEPTIDES.
CC ProDom; PD005617; Natr_peptide; 1.
CC SMART; SM00183; NAT_PEP; 1.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC K0M Hormone; Signal; Vasoactive.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 113
FT PEPTIDE 116 140 Atrial natriuretic factor.
FT DISULFID 119 135 By similarity.
SQ SEQUENCE 140 AA; 15577 MW; 5F2D214FA560DB0F CRC64;

Query Match 82.4%; Score 56; DB 1; Length 140;
Best Local Similarity 58.8%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGKXXSXXC 17
Db 119 CFGARMDRIGNASGLGC 135

RESULT 14
ANF_RANCA
ID ANF_RANCA STANDARD; PRT; 145 AA.
AC P18909;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANF).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
OC Aquarana.
OC NCB1_TaxID=8400;
OXX [1]
RN NUCLEOTIDE SEQUENCE.
RA Kojima M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PROTEIN SEQUENCE OF 122-145.
RX TISSUE=Heart;
RC MEDLINE=89025806; Pubmed=2972279;
RA Sakata J., Kangawa K., Matsuo H.;
RT "Identification of new atrial natriuretic peptides in frog heart.";
RL Biochem. Biophys. Res. Commun. 155:1338-1345(1988).
CC -1- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; D01043; BAA00850.1; -; mRNA.
DR PIR; JQ0947; JQ0947.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; At_natriurtcep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005107; At_natriurtcep; 1.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 119
FT PEPTIDE 122 145 Atrial natriuretic factor.
FT DISULFID 125 141
SQ SEQUENCE 145 AA; 15934 MW; 01EB3B979529405 CRC64;

Query Match 82.4%; Score 56; DB 1; Length 145;
Best Local Similarity 58.8%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
   ||| ||||| |||
DB 125 CFGSRIDRIGAGSGMGC 141

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RESULT 15
05XPR8_RANRI
ID 05XPR8_RANRI PRELIMINARY; PRT; 145 AA.
AC 05XPR8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Atrial natriuretic factor.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
OC Pelophylax.
OX NCBI_TaxID=8406;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Vassilopoulos A., Gaitanaki C., Papazafiri P., Beis I.;
RT "Expression of atrial natriuretic factor (ANF) in Rana ridibunda
RT perfused heart, during oxidative and mechanical stresses.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY743415; AAU93955.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005107; At_natriurtcep; 1.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT CHAIN 116 145 atrial natriuretic factor.
SQ SEQUENCE 145 AA; 15909 MM; 298F242F12B74A3E CRC64;

Query Match 82.4%; Score 56; DB 2; Length 145;
Best Local Similarity 58.8%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```


Qy 1 CFGXXXDRIGXXSXGC 17
| | | | | | | | | |
Db 125 CFGSRIDRIGASGMGC 141

RESULT 16
Q7T1Q2 ORYLA
ID Q7T1Q2_ORYLA PRELIMINARY; PRT; 146 AA.
Q7T1Q2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE B-type natriuretic peptide.
GN Name=bnp;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Inoue K., Takei Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB099700; BAC79151.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 146 AA; 16455 MW; E0EA2C0C70DAD51F CRC64;

Query Match 82.4%; Score 56; DB 2; Length 146;
Best Local Similarity 58.8%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
| | | | | | | | | |
Db 121 CFGRRMDRIGSMSSLC 137

RESULT 17
ANFB_ACITR STANDARD; PRT; 150 AA.
ID ANFB_ACITR
AC P83965;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Brain natriuretic peptide precursor (B-type natriuretic peptide).
GN Name=BNP;
OS Acipenser transmontanus (White sturgeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
OC Acipenser.
OX NCBI_TaxID=7904;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RC TISSUE=Heart ventricle;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
sturgeon: identification of BNP in fish lineage."
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological

CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Atrium and ventricle, and to a lesser extent
CC in brain.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB087729; BAD02836.1; -; mRNA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 25 Potential.
FT PROPEP 26 ?
FT PEPTIDE 150 Brain natriuretic peptide.
FT DISULFID 123 139 By similarity.
SQ SEQUENCE 150 AA; 16758 MW; AD5AA59C0BC292AB CRC64;

Query Match 82.4%; Score 56; DB 1; Length 150;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
| | | | | | | | | |
Db 123 CFGRRIDRIGSMSSALGC 139

RESULT 18
Q90X61_BUFMA
ID Q90X61_BUFMA PRELIMINARY; PRT; 159 AA.
AC Q90X61;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Atrial natriuretic peptide.
GN Name=ANP;
OS Bufo marinus (Giant toad) (Cane toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Bufonidae; Bufo.
OX NCBI_TaxID=8386;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22489717; PubMed=12601618; DOI=10.1086/344740;
RA Donald J.A., Meier S.K., Riddell S.;
RT "Toad atrial natriuretic peptide: cDNA cloning and functional analysis
in isolated perfused kidneys."
RL Physiol. Biochem. Zool. 75:617-626(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donald J.A., Riddell S.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF429999; AAL27433.3; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
KW Vasoactive.
SQ SEQUENCE 159 AA; 17418 MW; 0C06AEF07F12131A CRC64;

Query Match 82.4%; Score 56; DB 2; Length 159;

Best Local Similarity 58.8%; Pred. No. 0.00064;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXXRIGXXSXGC 17
Db 128 CFGSRIDRIGAGSGMGC 144

RESULT 19
ANFC CHICK STANDARD; PRT; 22 AA.
AC P21805;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-type natriuretic peptide (CNP).
GN Name=NPPC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91113186; PubMed=1989595;
RA Arimura J.J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation and identification of C-type natriuretic peptide in chicken brain."
RL Biochem. Biophys. Res. Commun. 174:142-148(1991).
CC -!- FUNCTION: Vasorelaxant activity. Has a CGMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR: JT0581; JT0581.
DR Ensembl; ENSGALG00000004572; Gallus gallus.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR PRINTS; PR00712; BNATPEPTIDE.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Vasoactive.
FT DISULFID 6 22
SQ SEQUENCE 22 AA; 2244 MW; FC2A4706D8DAC025 CRC64;
Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXXRIGXXSXGC 17
Db 6 CFGVKLDRIGSMGLGC 22
RESULT 20
Q4SND6_TETNG PRELIMINARY; PRT; 25 AA.
AC Q4SND6;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Chromosome 8 SCAF14543, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00015340001;

OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalll Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01014543; CAF97846.1; -; Genomic_DNA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2727 MW; 8D77FED313F74A90 CRC64;
Query Match 80.9%; Score 55; DB 2; Length 25;
Best Local Similarity 58.8%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXXRIGXXSXGC 17
Db 9 CFGKLDRIGSMGLGC 25
RESULT 21
ANF ANGJA STANDARD; PRT; 27 AA.
AC P18144;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Atrial natriuretic factor (ANF) (Atrial natriuretic peptide) (ANP).
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Heart atrium;
RX MEDLINE=90026430; PubMed=2529857;
RA Takei Y., Takahashi A., Watanabe T.X., Nakajima K., Sakakibara S.;
RT "Amino acid sequence and relative biological activity of eel atrial
RT natriuretic peptide.";
RL Biochem. Biophys. Res. Commun. 164:537-543(1989).

```
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A33431; A33431.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; At_natriurtcep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005107; At_natriurtcep; 1.
DR ProDom; PD005617; Natr_peptide; 2.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPIDE; 1.
KW Direct protein sequencing; Hormone; Vasoactive.
FT DISULFID 7 23
SQ SEQUENCE 27 AA; 2792 MW; 9EF510CCF282B4D CRC64;

Query Match 80.9%; Score 55; DB 1; Length 27;
Best Local Similarity 58.8%; Pred. No. 0.00021;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXXSXXGC 17
Db 7 CFGKLDRIIGSYSGLC 23

RESULT 22
Q9QZ96_CAVPO PRELIMINARY; PRT; 33 AA.
ID Q9QZ96_CAVPO PRELIMINARY; PRT; 33 AA.
AC Q9QZ96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-type natriuretic peptide/factor (Fragment).
GN Name=CNP;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hartley; TISSUE=Heart;
RA Aguan K., Thompson L., Weiner C.P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193572; AAF04122.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPIDE; 1.
KW Vasoactive.
FT CHAIN <1 33 C-type natriuretic peptide/factor active
peptide.
```

```
FT NON TER 1 1
SQ SEQUENCE 33 AA; 3445 MW; C4DE805DF7E762AE CRC64;

Query Match 80.9%; Score 55; DB 2; Length 33;
Best Local Similarity 58.8%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXXSXXGC 17
Db 17 CFGKLDRIIGSYSGLC 33 ✓

RESULT 23
NFNP_PSEPC
ID NFNP_PSEPC STANDARD; PRT; 37 AA.
AC P82972;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Natriuretic peptide PNP.
OS Pseudocerastes persicus (Persian horned viper) (False horned viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Pseudocerastes.
OX NCBI_TaxID=47769;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
SPECIFICITY, MASS SPECTROMETRY, AND DISULFIDE BOND.
RC TISSUE=Venom;
RX PubMed=14741349; DOI=10.1016/S0014-5793(03)01455-8;
RA Amininasab M., Elmi M.M., Endlich N., Endlich K., Parekh N.,
RA Naderi-Manesh H., Schaller J., Mostafavi H., Sattler M.,
RA Sarbolouki M.N., Muhle-Goll C.;
RT "Functional and structural characterization of a novel member of the
RT natriuretic family of peptides from the venom of Pseudocerastes
RT persicus."
RL FEBS Lett. 557:104-108 (2004).
CC -!- FUNCTION: Increases urine flow and decreases blood pressure when
CC administered to rats by intravenous injection. Inhibits thrombin-
CC induced platelet aggregation. Has a cGMP-stimulating activity.
CC -!- SUBUNIT: Monomer. Binds to the NPR-A receptor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=3941.5; MW_ERR=0.17; METHOD=Electrospray;
CC RANGE=1-37; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR GO; GO:0005576; C:extracellular region; IDA.
DR GO; GO:0030146; P:diuresis; IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure; IDA.
DR GO; GO:0009405; P:pathogenesis; IDA.
DR GO; GO:0030828; P:positive regulation of cGMP biosynthesis; IDA.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005107; At_natriurtcep; 1.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPIDE; 1.
KW Direct protein sequencing; Toxin; Vasoactive.
FT DISULFID 14 30
SQ SEQUENCE 37 AA; 3944 MW; AD7BE649AD480BA6 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 37;
```


Best Local Similarity 58.8%; Pred. No. 0.00028;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| ||| |||
Db 14 CFGHKIDRIGSHSGLGC 30

RESULT 24
Q7LZ09_VIPLE
ID Q7LZ09_VIPLE PRELIMINARY; PRT; 38 AA.
AC Q7LZ09;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE lebetin 2 isoform alpha.
OS Vipera lebetina (Elephant snake) (Leventine viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Macrovipera.
OX NCBI_TaxID=8709;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96354866; PubMed=8769304; DOI=10.1016/0014-5793(96)00774-0;
RA Barbouche R., Marrakchi N., Mansuelle P., Krifi M., Fenouillet E.,
RA Rochat H., El Ayeb M.;
RT "Novel anti-platelet aggregation polypeptides from Vipera lebetina
venom: isolation and characterization.";
RL FEBS Lett. 392:6-10(1996).
DR PIR; S71381; S71381.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 38 AA; 3945 MW; 831FASCB9B1B09377 CRC64;

Query Match 80.9%; Score 55; DB 2; Length 38;
Best Local Similarity 58.8%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| ||| |||
Db 14 CFGHKIDRIGSHSGLGC 30

RESULT 25
Q4S797_TETNG
ID Q4S797_TETNG PRELIMINARY; PRT; 101 AA.
AC Q4S797;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Chromosome 1 SCARF4716, whole genome shotgun sequence.
GN ORFNames=GSTENG00022908001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jalllon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfaila G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01014716; CAG03485.1; -; Genomic_DNA.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 101 AA; 11398 MW; 31CA29F92812C3D0 CRC64;

Query Match 80.9%; Score 55; DB 2; Length 101;
Best Local Similarity 58.8%; Pred. No. 0.0007;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| ||| |||
Db 85 CFGHKMDRIGTISGMGC 101

RESULT 26
ANFB_BOVIN
ID ANFB_BOVIN STANDARD; PRT; 103 AA.
AC P13204;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic
DE peptide; Aldosterone secretion inhibitory factor (ASIF); Brain
DE natriuretic peptide 26 (BNP-26)].
GN Name=NPPB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90114187; PubMed=2532709;
RA Nguyen T.T., Lazure C., Babinski K., Chretien M., de Lean A., Ong H.;
RT "Purification and primary structure of pro-aldosterone secretion
RT inhibitory factor from bovine adrenal chromaffin cells.";
RL Mol. Endocrinol. 3:1823-1829(1989).
RN [2]
RP PROTEIN SEQUENCE OF 69-103.
RX MEDLINE=89136947; PubMed=2537187;
RA Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;
RT "Aldosterone secretion inhibitory factor: a novel neuropeptide in
RT bovine chromaffin cells.";
RL Endocrinology 124:1591-1593(1989).
CC -1- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the

```
CC body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
CC levels than ANP.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A41403; A41403.
DR InterPro; IPR002408; Br_natriureticpep.
DR InterPro; IPR000663; Natri_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natri_peptide; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Vasoactive.
FT CHAIN 1 103 Gamma-brain natriuretic peptide.
FT PEPTIDE 69 103 Aldosterone secretion inhibitory factor.
FT PEPTIDE 78 103 Brain natriuretic peptide 26.
FT DISULFID 81 97
SQ SEQUENCE 103 AA; 11249 MW; 40209204AFE3851D CRC64;

Query Match 80.9%; Score 55; DB 1; Length 103;
Best Local Similarity 58.8%; Pred. No. 0.00071;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXSXXGC 17
Db 81 CFGRRLDRIIGSLGLGC 97

RESULT 27
Q9GLK5_FELCA PRELIMINARY; PRT; 112 AA.
ID Q9GLK5_FELCA
AC Q9GLK5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Brain natriuretic peptide (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felis.
OC NCBI_TaxID=9685;
OX
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu Z.L., Wiedmeyer C.E., Solter P.F., Sisson D.D.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251261; AAG13660.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriureticpep.
DR InterPro; IPR000663; Natri_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natri_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 1 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12083 MW; 580224F12984FFB2 CRC64;

Query Match 80.9%; Score 55; DB 2; Length 112;
Best Local Similarity 58.8%; Pred. No. 0.00077;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

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Qy 1 CFGXXXDRIGXSXXGC 17
Db 90 CFGRRLDRIIGSLGLGC 106

RESULT 28
ANFC_SCYCA STANDARD; PRT; 115 AA.
ID ANFC_SCYCA
AC P23259;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE C-type natriuretic peptide prohormone precursor (CNP-115) [Contains:
DE CNP-39; CNP-38; CNP-22].
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Heart atrium, and Heart ventricle;
RX MEDLINE=91243822; PubMed=1828036; DOI=10.1016/0014-5793(91)80505-W;
RA Suzuki R., Takahashi A., Hazon N., Takei Y.;
RT "Isolation of high-molecular-weight C-type natriuretic peptide from
RT the heart of a cartilaginous fish (European dogfish, Scyliorhinus
RT canicula)."
RL FEBS Lett. 282:321-325(1991).
CC -!- FUNCTION: Vaso relaxant activity. Has a cGMP-stimulating activity
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: CNP-115 is differentially processed to produce
CC CNP-38 and CNP-39 in the heart and CNP-22 in the brain.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; S15822; S15822.
DR InterPro; IPR002406; C_natriureticpep.
DR InterPro; IPR000663; Natri_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natri_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Vasoactive.
FT CHAIN 1 115 C-type natriuretic peptide prohormone.
FT PEPTIDE 77 115 CNP-39.
FT PEPTIDE 78 115 CNP-38.
FT PEPTIDE 94 115 CNP-22.
FT DISULFID 99 115 By similarity.
SQ SEQUENCE 115 AA; 12885 MW; 49AE7200EE4C7F8A CRC64;

Query Match 80.9%; Score 55; DB 1; Length 115;
Best Local Similarity 58.8%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXSXXGC 17
Db 99 CFGVLDRIIGAMSLGLGC 115

RESULT 29
ANFD_RANCA STANDARD; PRT; 118 AA.
ID ANFD_RANCA
AC P40756;
DT 01-FEB-1995 (Rel. 31, Created)
```

DT 01-FEB-1995 (Rel. 31, last sequence update)
 DT 10-MAY-2005 (Rel. 47, last annotation update)
 DE C-type natriuretic peptide-2 precursor (CNP II).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
 OC Aquarana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94230409; PubMed=8175740;
 RA Kojima M., Ohyama Y., Miyamoto K., Minamino N., Kangawa K., Matsuo H.;
 RT "Cloning and characterization of a novel natriuretic peptide in frog
 (Rana catesbeiana).";
 RL J. Biol. Chem. 269:13136-13140(1994).
 CC -1- FUNCTION: Exhibits natriuretic and vasodepressor activity. Has a
 CC CGMP-stimulating activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; D17414; BAA04236.1; -; mRNA.
 DR PIR; B54119; B54119.
 DR InterPro; IPR002406; C_natriurtcpep.
 DR InterPro; IPR000663; Natr_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00713; CNATPEPTIDE.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR ProDom; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Hormone; Signal; Vasoactive.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 94
 FT PEPTIDE 97 118 C-type natriuretic peptide-2.
 FT DISULFID 102 118 By similarity.
 SQ SEQUENCE 118 AA; 13136 MW; F091C3C4AD707603 CRC64;
 Query Match 80.9%; Score 55; DB 1; Length 118;
 Best Local Similarity 58.8%; Pred. No. 0.00081;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXXRIGXXSXXGC 17
 DB 102 CFGKLDRIGAMSGLC 118
 RESULT 30
 ANFC4_FUGRU STANDARD; PRT; 120 AA.
 ID ANFC4_FUGRU
 AC O805D3;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, last sequence update)
 DT 10-MAY-2005 (Rel. 47, last annotation update)
 DE C-type natriuretic peptide-4 precursor.
 DE Name=cnp-4;
 GN Name=cnp-4;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA PubMed=12893874; DOI=10.1073/pnas.1632368100;
 RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takei Y.;

RT "Four functionally distinct C-type natriuretic peptides found in fish
 RT reveal evolutionary history of the natriuretic peptide system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
 CC -1- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
 CC CGMP-stimulating activity. May help to regulate body fluid
 CC homeostasis in a variety of aquatic environments.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AB089938; BAC57074.1; -; mRNA.
 DR Ensembl; SINFUG00000151691; Fugu rubripes.
 DR InterPro; IPR002406; C_natriurtcpep.
 DR InterPro; IPR000663; Natr_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00713; CNATPEPTIDE.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR ProDom; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Hormone; Signal; Vasoactive.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 94
 FT PEPTIDE 97 120 C-type natriuretic peptide-4.
 FT DISULFID 104 120 By similarity.
 SQ SEQUENCE 120 AA; 13504 MW; 27233AEC1FA3313E CRC64;
 Query Match 80.9%; Score 55; DB 1; Length 120;
 Best Local Similarity 58.8%; Pred. No. 0.00082;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXXRIGXXSXXGC 17
 DB 104 CFGHKMDRIGTISGMGC 120
 RESULT 31
 ANFB_MOUSE STANDARD; PRT; 121 AA.
 ID ANFB_MOUSE
 AC P40753;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 10-MAY-2005 (Rel. 47, last annotation update)
 DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic
 DE peptide; Brain natriuretic peptide (BNP)].
 DE Name=Nppb;
 GN Name=Nppb;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RX MEDLINE=94237953; PubMed=8182124;
 RA Ogawa Y., Itoh H., Tamura N., Suga S., Yoshimasa T., Uehira M.,
 RA Matsuda S., Shiono S., Nishimoto H., Nakao K.;
 RT "Molecular cloning of the complementary DNA and gene that encode mouse
 RT brain natriuretic peptide and generational DNA of transgenic mice that
 RT overexpress the brain natriuretic peptide gene.";
 RL J. Clin. Invest. 93:1911-1921(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RX MEDLINE=93238395; PubMed=8097440;
 RA Steinhilber M.E.;
 RT "Structure, expression, and genomic mapping of the mouse natriuretic
 RT peptide type-B gene.";

RL Circ. Res. 72:984-992(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=PA0753-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=PA0753-2; Sequence=VSP_000263;
CC -!- TISSUE SPECIFICITY: Expressed abundantly in the ventricle, and in
CC a lesser extent in the atrium.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; D16497; BAA03948.1; -; Genomic_DNA.
DR EMBL; S58667; AAB26344.2; -; Genomic_DNA.
DR EMBL; BC061165; AAH61165.1; -; mRNA.
DR PIR; I49548; I49548.
DR Ensemble; ENSMUSG0000029019; Mus musculus.
DR MGI; MGI:97368; Npnb.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR002408; Br_natriurecep.
DR InterPro; IPR006663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Alternative splicing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 26 By similarity.
FT PEPTIDE 27 121 Gamma-brain natriuretic peptide.
FT PEPTIDE 77 121 Brain natriuretic peptide.
FT DISULFID 99 115 By similarity.
FT VARSPLIC 43 43 Missing (in isoform short).
FT /FTId=VSP_000263.
FT CONFLICT 27 27 Y -> H (in Ref. 2).
FT CONFLICT 71 71 P -> L (in Ref. 2).
SQ SEQUENCE 121 AA; 13756 MW; 4F62AC9445E293B9 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 121;

Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXDRIGXXSXGC 17
Db 99 CFGHKIDRIGSVSLGC 115
RESULT 32
ANFB_RAT
ID ANFB_RAT STANDARD; PRT; 121 AA.
AC P13205;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Natriuretic peptides B precursor (Iso-ANP) [Contains: Gamma-brain
DE natriuretic peptide; Brain natriuretic peptide 45 (BNP-34) (5 kDa
DE cardiac natriuretic peptide)].
GN Name=Npnb;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=89193742; PubMed=2522776;
RX Kojima M., Minamino N., Kangawa K., Matsuo H.;
RA "Cloning and sequence analysis of cDNA encoding a precursor for rat
RT brain natriuretic peptide."
RL Biochem. Biophys. Res. Commun. 159:1420-1426(1989).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=90365739; PubMed=214113;
RX Roy R.N., Flynn T.G.;
RA "Organization of the gene for iso-rANP, a rat B-type natriuretic
RT peptide."
RL Biochem. Biophys. Res. Commun. 171:416-423(1990).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=92123224; PubMed=1837590;
RX Dagnino L., Drouin J., Nemer M.;
RA "Differential expression of natriuretic peptide genes in cardiac and
RT extracardiac tissues."
RL Mol. Endocrinol. 5:1292-1300(1991).
RN [4]
RN PROTEIN SEQUENCE OF 27-121.
RP MEDLINE=89374230; PubMed=2673236;
RX Abuyara M., Hino J., Minamino N., Kangawa K., Matsuo H.;
RA "Isolation and identification of rat brain natriuretic peptides in
RT cardiac atrium."
RL Biochem. Biophys. Res. Commun. 163:226-232(1989).
RN [5]
RN PROTEIN SEQUENCE OF 77-121.
RP TISSUE=Heart;
RC MEDLINE=89374231; PubMed=2528349;
RX Kambayashi Y., Nakao K., Itoh H., Hosoda K., Saito Y., Yamada T.,
RA Mukoyama M., Arai H., Shirikami G., Suga S.-I., Ogawa Y.,
RA Jougasaki M., Minamino N., Kangawa K., Matsuo H., Inouye K., Imura H.;
RA "Isolation and sequence determination of rat cardiac natriuretic
RT peptide."
RL Biochem. Biophys. Res. Commun. 163:233-240(1989).
RN [6]
RN PROTEIN SEQUENCE OF 77-121.
RP MEDLINE=89286593; PubMed=2525380;
RX Flynn T.G., Brar A., Tremblay L., Sarda I., Lyons C., Jennings D.B.;
RA "Isolation and characterization of iso-rANP, a new natriuretic peptide
RT from rat atria."
RL Biochem. Biophys. Res. Commun. 161:830-837(1989).
RN [7]
RN PROTEIN SEQUENCE OF 99-115.
RP MEDLINE=89286579; PubMed=2525379;
RX Itoh H., Nakao K., Kambayashi Y., Hosoda K., Saito Y., Yamada T.,

RA Mukoyama M., Arai H., Shirakami G., Suga S.-I., Yoshida I., Inouye K.,
RA Imura H.,
RT "Occurrence of a novel cardiac natriuretic peptide in rats." J. Biol. Chem. 267:1151-1154 (1992).
RL Biochem. Biophys. Res. Commun. 161:732-739(1989).
CC -1- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
CC levels than ANP.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M25297; AAA57269.1; -; mRNA.
DR EMBL; M60731; AAA41456.1; -; Genomic_DNA.
DR EMBL; M60266; AAA41455.1; -; Genomic_DNA.
DR PIR; A30162; A30162.
DR Ensemble; ENSRNOG0000008141; Rattus norvegicus.
DR RGD; 3194; Npfb.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 26
FT PEPTIDE 27 121 Gamma-brain natriuretic peptide.
FT PEPTIDE 77 121 Brain natriuretic peptide 45.
FT DISULFID 99 115
FT CONFLICT 15 15 L -> V (in Ref. 2).
FT CONFLICT 120 120 L -> Q (in Ref. 6).
SQ SEQUENCE 121 AA; 13656 MW; B5D4151ED18C7294 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
Db 99 CFGQKIDRIGAVSRLGC 115

RESULT 33
ANFC4_ORYLA STANDARD; PRT; 121 AA.
ID ANFC4_ORYLA
AC Q80017;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-4 precursor.
GN Name=cnp-4;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takei Y.,
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -1- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC cGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain, spinal cord, spleen, heart and fin, and
CC to a lower extent in gill and ovary.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB091699; BAC65998.1; -; mRNA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22
FT PROPEP 23 94 Potential.
FT PEPTIDE 97 121 By similarity.
FT DISULFID 105 121 C-type natriuretic peptide-4.
FT DISULFID 105 121 By similarity.
SQ SEQUENCE 121 AA; 13457 MW; EFD7ED534B137009 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
Db 105 CFGHKMDRIGTISGMGC 121

RESULT 34
Q794A8_MOUSE
ID Q794A8_MOUSE PRELIMINARY; PRT; 121 AA.
AC Q794A8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Brain natriuretic peptide.
GN Name=BNP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HMI/Msf;
RA Liu Y., Kitano T., Koide T., Shirosaki T., Moriwaki K., Saitou N.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039051; BAB68575.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 121 AA; 13739 MW; BD608CB65CDB83AA CRC64;

Query Match 80.9%; Score 55; DB 2; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXGC 17
||| ||| |
Db 99 CFGHKIDRIGSVSRLGC 115

RESULT 35
Q91V40 MUSSI
ID Q91V40 MUSSI PRELIMINARY; PRT; 121 AA.
AC Q91V40;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Brain natriuretic peptide.
GN Name=BNP;
OS Mus spicilegus (Steppe mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ZBN;
RA Liu Y., Kitano T., Koide T., Shirotani T., Moriwaki K., Saitou N.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039053; BAB68577.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 121 AA; 13739 MW; BD608CB65CDB83AA CRC64;

Query Match 80.9%; Score 55; DB 2; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXGC 17
||| ||| |
Db 99 CFGHKIDRIGSVSRLGC 115

RESULT 36
Q54AE9 MOUSE
ID Q54AE9 MOUSE PRELIMINARY; PRT; 121 AA.
AC Q54AE9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Brain natriuretic peptide (Adult male heart cDNA, RIKEN full-length enriched library, clone:1010001K23 product:natriuretic peptide type B, DE full insert sequence).
GN Name=Nppb; Synonyms=BNP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CAST/Ei, N1L/Msf, and C57BL/10SnJ;
RA Liu Y., Kitano T., Koide T., Shirotani T., Moriwaki K., Saitou N.;

RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki A., Yamana I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kasasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;


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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039047; BAB68571.1; -; Genomic_DNA.
DR EMBL; AB039052; BAB68576.1; -; Genomic_DNA.
DR EMBL; AK003128; BAB22588.1; -; mRNA.
DR EMBL; AB039044; BAB68568.1; -; Genomic_DNA.
DR MGI; MGI:97368; Npdp.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR002408; Br_natriureticp.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 121 AA; 13756 MW; 4F62AC9445E293B9 CRC64;

Query Match 80.9%; Score 55; DB 2; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
DB 99 CFGHKIDRIGSVSRLGC 115

RESULT 37
O55086_MOUSE PRELIMINARY; PRT; 121 AA.
ID O55086_MOUSE PRELIMINARY; PRT; 121 AA.
AC O55086;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Brain natriuretic peptide.
GN Name=BNP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX MEDLINE=94237953; PubMed=8182124;
RA Ogawa Y., Itoh H., Tamura N., Suga S., Yoshimasa T., Uehira M.,
RA Matsuda S., Shiono S., Nishimoto H., Nakao K.;
RT "Molecular cloning of the complementary DNA and gene that encode mouse
RT brain natriuretic peptide and generation of transgenic mice that
RT overexpress the brain natriuretic peptide gene.";
RL J. Clin. Invest. 93:1911-1921(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX MEDLINE=97031884; PubMed=8877790; DOI=10.1006/jmcc.1996.0170;
RA Tamura N., Ogawa Y., Yasoda A., Nakao K.;
RT "Two cardiac natriuretic peptide genes (atrial natriuretic peptide and
RT brain natriuretic peptide) are organized in tandem in the mouse and
RT human genomes.";
RL J. Mol. Cell. Cardiol. 28:1811-1815(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B6M/2msf, BLG2/Msf, MSM/Msf, pgn2, and SWN/Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; D82049; BAA24159.1; -; Genomic_DNA.
DR EMBL; AB039045; BAB68569.1; -; Genomic_DNA.
DR EMBL; AB039046; BAB68570.1; -; Genomic_DNA.
DR EMBL; AB039048; BAB68572.1; -; Genomic_DNA.
DR EMBL; AB039050; BAB68574.1; -; Genomic_DNA.
DR EMBL; AB039049; BAB68573.1; -; Genomic_DNA.
DR Ensembl; ENSMUSG0000029019; Mus musculus.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriureticp.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 121 AA; 13730 MW; 54781D3F445283B8 CRC64;

Query Match 80.9%; Score 55; DB 2; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
DB 99 CFGHKIDRIGSVSRLGC 115

RESULT 38
ANFC1_FUGRU STANDARD; PRT; 126 AA.
ID ANFC1_FUGRU STANDARD; PRT; 126 AA.
AC Q805D6;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-1 precursor.
GN Name=cnp-1;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takei Y.;

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RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -|- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB089935; BAC57071.1; -; mRNA.
DR Ensembl; SINFRUG00000146920; Fugu rubripes.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 102 By similarity.
FT PEPTIDE 105 126 C-type natriuretic peptide-1.
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 14068 MW; DF3F235C2C8D4FF6 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXSXXGC 17
Db 110 CFGKLDRIGSMSG LGC 126

RESULT 39
ANFC2_ORYLA STANDARD; PRT; 126 AA.
ID ANFC2_ORYLA
AC Q8AYR5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-2 precursor.
GN Name=cnp-2;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takei Y.;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -|- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Brain and spinal cord.
CC -|- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC removed.
CC -----
DR EMBL; AB081456; BAC15761.1; -; mRNA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 100 By similarity.
FT PEPTIDE 103 126 C-type natriuretic peptide-2.
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECB0F92 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXSXXGC 17
Db 110 CFGMKMDRIGSISGLGC 126

RESULT 40
ANFC_BOVIN STANDARD; PRT; 126 AA.
ID ANFC_BOVIN
AC P53206;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor (SVSP15) [Contains: CNP-22; CNP-
DE 29; CNP-53].
GN Name=NPPC;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94280621; PubMed=8011167;
RA Hosang K.K., Scheit K.K.;
RT "cDNA cloning identified a calmodulin-binding protein in bovine
RT seminal plasma as bovine C-type natriuretic peptide.";
RL DNA Cell Biol. 13:409-417(1994).
CC -|- FUNCTION: Vasoelaxant activity. Has a CGMP-stimulating activity.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Z48478; CAA88369.1; -; mRNA.
DR EMBL; Z48477; CAA88368.1; -; mRNA.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.

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FT PROPEP      24      72      Potential.
FT PEPTIDE     74      126     CNP-53 (By similarity).
FT PEPTIDE     98      126     CNP-29 (By similarity).
FT PEPTIDE    105      126     CNP-22.
FT DISULFID    110      126     By similarity.
SQ SEQUENCE    126 AA; 13291 MW; 31EDF80F4A98DD77 CRC64;

Query Match      80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY      1 CFXGXXDRIGXXSXGC 17
      ||| ||| ||| |||
DB      110 CFGLKLDRI GSMGLGC 126

RESULT 41
ANFC_HUMAN
ID _ANFC_HUMAN      STANDARD;      PRT;      126 AA.
AC P23582;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [contains: CNP-22; CNP-29; CNP-
DE 53].
GN Name=NPPC; Synonyms=CNPF2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91207363; PubMed=2018508;
RA Tawaragi Y., Fuchimura K., Tanaka S., Minamino N., Kangawa K.,
RA Matsuo H.;
RT "Gene and precursor structures of human C-type natriuretic peptide.";
RL Biochem. Biophys. Res. Commun. 175:645-651(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92275775; PubMed=1339402;
RA Ogawa Y., Nakao K., Nakagawa O., Komatsu Y., Hosoda K., Suga S.,
RA Arai H., Nagata K., Yoshida N., Imura H.;
RT "Human C-type natriuretic peptide. Characterization of the gene and
RT peptide.";
RL Hypertension 19:809-813(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROTEIN SEQUENCE OF 98-126.
RX MEDLINE=93112033; PubMed=1472040;
RA Ishizaka Y., Kangawa K., Minamino N., Ishii K., Takano S., Eto T.,
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RA Matsuo H.;
RT "Isolation and identification of C-type natriuretic peptide in human
RT monocytic cell line, THP-1.";
RL Biochem. Biophys. Res. Commun. 189:697-704(1992).
CC -!- FUNCTION: Vaso relaxant activity. Has a cGMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC -----
DR EMBL; M64710; AAA35703.1; -; Genomic DNA.
DR EMBL; D90337; BAA14351.1; -; Genomic DNA.
DR EMBL; BC069120; AAH69120.1; -; mRNA.
DR PIR; J10567; AMHUC.
DR PDB; 1JDP; X-ray; H=105-126.
DR Ensembl; ENSG00000163273; Homo sapiens.
DR HGNC; HGNC:7941; NPPC.
DR MIM; 600296; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0008217; P:regulation of blood pressure; NAS.
DR GO; GO:0019229; P:regulation of vasoconstriction; NAS.
DR InterPro; IPR002406; C natriuretic pep.
DR InterPro; IPR000663; Natriuretic peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natri peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC PEPTIDE; 1.
KW 3D-structure; Direct protein sequencing; Hormone; Polymorphism;
KW Signal; Vasoactive.
FT SIGNAL      1      23      Potential.
FT PROPEP      24      72
FT PEPTIDE     74      126     CNP-53.
FT PEPTIDE     98      126     CNP-29.
FT PEPTIDE    105      126     CNP-22.
FT DISULFID    110      126     By similarity.
FT VARIANT      82      82     R -> Q (in dbSNP:52677).
FT          /FTId=VAR_014583.
SQ SEQUENCE    126 AA; 13246 MW; 58FE6E57868F9A2D CRC64;

Query Match      80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY      1 CFXGXXDRIGXXSXGC 17
      ||| ||| ||| |||
DB      110 CFGLKLDRI GSMGLGC 126

RESULT 42
ANFC_MOUSE
ID _ANFC_MOUSE      STANDARD;      PRT;      126 AA.
AC Q61839;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [contains: CNP-22; CNP-29; CNP-
DE 53].
GN Name=Nppc; Synonyms=Cnp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=95213034; PubMed=7698765;
```


RA Ogawa Y., Itoh H., Yoshitake Y., Inoue M., Yoshimasa T., Serikawa T.,
RA Nakao K.;
RT "Molecular cloning and chromosomal assignment of the mouse C-type
RT natriuretic peptide (CNP) gene (Nppc): comparison with the human CNP
RT gene (NPPC).";
RL Genomics 24:383-387(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX MEDLINE=97053441; PubMed=8897953;
RA Huang H., Acuff C.G., Steinhilber M.E.;
RT "Isolation, mapping, and regulated expression of the gene encoding
RT mouse C-type natriuretic peptide.";
RL Am. J. Physiol. 271:H1565-H1575(1996).
CC -!- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC -----
CC EMBL; D28873; BAA06028.1; -; Genomic_DNA.
CC EMBL; U62939; AAB61717.1; -; Genomic_DNA.
CC PIR; A55688; A55688.
CC Ensembl; ENSMUSG00000026241; Mus musculus.
DR MGI; MGI:97369; Npdc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005184; F:neuropeptide hormone activity; TAS.
DR GO; GO:0005102; F:receptor binding; IDA.
DR GO; GO:0006182; P:cGMP biosynthesis; IDA.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 72
FT PEPTIDE 74 126 CNP-53 (By similarity).
FT PEPTIDE 98 126 CNP-29 (By similarity).
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 13320 MW; 8F65B1C4E82F0ACB CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXGC 17
||| ||||| |
DB 110 CFGKLDRIGSMGLGC 126

RESULT 43
ANFC_PIG STANDARD; PRT; 126 AA.
ID ANFC_PIG
AC P18104; P21806;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-
DE 53].
GN Name=NPPC; Synonyms=CNP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.

OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91054475; PubMed=2146957;
RA Tawaragi Y., Fuchimura K., Nakazato H., Tanaka S., Minamino N.,
RA Kangawa K., Matsuo H.;
RT "Gene and precursor structure of porcine C-type natriuretic peptide.";
RL Biochem. Biophys. Res. Commun. 172:627-632(1990).
RN [2]
RP PROTEIN SEQUENCE OF 74-126.
RC TISSUE=Brain;
RX MEDLINE=90343827; PubMed=2383278;
RA Minamino N., Kangawa K., Matsuo H.;
RT "N-terminally extended form of C-type natriuretic peptide (CNP-53)
RT identified in porcine brain.";
RL Biochem. Biophys. Res. Commun. 170:973-979(1990).
RN [3]
RP PROTEIN SEQUENCE OF 105-126.
RC TISSUE=Brain;
RX MEDLINE=90241265; PubMed=2139780;
RA Sudoh T., Minamino N., Kangawa K., Matsuo H.;
RT "C-type natriuretic peptide (CNP): a new member of natriuretic peptide
RT family identified in porcine brain.";
RL Biochem. Biophys. Res. Commun. 168:863-870(1990).
CC -!- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC removed.
CC -----
CC EMBL; M64758; AAA31018.1; -; Genomic_DNA.
CC PIR; A36155; A36155.
CC InterPro; IPR002406; C_natriurtcep.
CC InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 72
FT PEPTIDE 74 126 CNP-53.
FT PEPTIDE 98 126 CNP-29 (By similarity).
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126
SQ SEQUENCE 126 AA; 13243 MW; E2474B2D4AABF4DD CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXGC 17
||| ||||| |
DB 110 CFGKLDRIGSMGLGC 126

RESULT 44
ANFC_RAT STANDARD; PRT; 126 AA.
ID ANFC_RAT
AC P55207;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-
DE 53].
GN Name=Nppc; Synonyms=Cnp;
OS Rattus norvegicus (Rat).

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91092420; PubMed=1702395; DOI=10.1016/0014-5793(90)80544-S;
RA Kojima M., Minamino N., Kangawa K., Matsuo H.;
RT "Cloning and sequence analysis of a cDNA encoding a precursor for rat
RT C-type natriuretic peptide (CNP).";
RL FEBS Lett. 276:209-213(1990).
CC -1- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed exclusively in brain.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
-----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; D90219; BAA14250.1; -; mRNA.
DR PIR; S12988; S12988.
DR Ensembl; ENSRNOG0000018854; Rattus norvegicus.
DR RGD; 620850; Nppc.
DR InterPro; IPR002406; C_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 potential.
FT PROPEP 24 72
FT PEPTIDE 74 126 CNP-53.
FT PEPTIDE 98 126 CNP-29 (By similarity).
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 13314 MW; 0957A0DB5BC82E08 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
Db 110 CFGKLDRIGSMGLGC 126

RESULT 45
ANFC_SHEEP STANDARD; PRT; 126 AA.
ID ANFC_SHEEP
AC P56283;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-
DE 53].
GN Name=NPFC; Synonyms=CNP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99236261; PubMed=10219521; DOI=10.1016/S0739-7240(99)00005-3;
RA Aitken G.D., Ratziis A.M., Yandle T.G., George P.M., Espiner E.A.,
RA Cameron V.A.;
RT "The characterization of ovine genes for atrial, brain, and C-type
```

```
RT natriuretic peptides.";
RL Domest. Anim. Endocrinol. 16:115-121(1999).
CC -1- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; AF037467; AAB92261.1; -; Genomic DNA.
DR InterPro; IPR002406; C_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 potential.
FT PROPEP 24 72
FT PEPTIDE 74 126 CNP-53 (By similarity).
FT PEPTIDE 98 126 CNP-29 (By similarity).
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 13317 MW; 83C21B3C49A8F18B CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
Db 110 CFGKLDRIGSMGLGC 126

RESULT 46
Q4ZG41 HUMAN PRELIMINARY; PRT; 126 AA.
ID Q4ZG41_HUMAN
AC Q4ZG41;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein NPFC.
GN Name=NPFC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kozlowski A., Spalding L., Tomlinson C.;
RT "The sequence of Homo sapiens BAC clone RP11-52C8.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC013435; AAX88912.1; -; Genomic DNA.
DR InterPro; IPR002406; C_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
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DR Pfam: PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPIDE; 1.
KW Hypothetical protein; Vasoactive.
SQ SEQUENCE 126 AA; 13246 MW; 58F6B657868F9A2D CRC64;

Query Match 80.9%; Score 55; DB 2; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 110 CFGKLDRIGSMGLGC 126

RESULT 47
Q544KS_MOUSE PRELIMINARY; PRT; 126 AA.
ID Q544KS_MOUSE PRELIMINARY;
AC Q544KS;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 16 days neonate cerebellum cDNA, RIKEN full-length enriched library,
clone:9630044D15 product:natriuretic peptide type C, full insert
sequence.
GN Name=Npc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Osato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK036176; BAC29333.1; -, mRNA.
DR MGI; MGI:97369; Nnpc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005184; F:neuropeptide hormone activity; TAS.
DR GO; GO:0005102; F:receptor binding; IDA.
DR GO; GO:0006182; P:cGMP biosynthesis; IDA.
KW Vasoactive.
SQ SEQUENCE 126 AA; 13320 MW; 8F65B1C4E82F0ACB CRC64;

Query Match 80.9%; Score 55; DB 2; Length 126;

Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 110 CFGKLDRIKSGSLGC 126

RESULT 48

ANFB_SHEEP STANDARD; PRT; 129 AA.
ID ANFB_SHEEP
AC 046541;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic peptide; Brain natriuretic peptide 29 (BNP-29); Brain natriuretic peptide 26 (BNP-26)].
GN Name=NPFB;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99236261; PubMed=10219521; DOI=10.1016/S0739-7240(99)00005-3;
RA Aitken G.D., Raizis A.M., Yandle T.G., George P.M., Espiner E.A., Cameron V.A.;
RT "The characterization of ovine genes for atrial, brain, and C-type natriuretic peptides.";
RL Domest. Anim. Endocrinol. 16:115-121(1999).
CC -1- FUNCTION: Acts as a cardiac hormone with a variety of biological actions including natriuresis, diuresis, vasorelaxation, and inhibition of renin and aldosterone secretion. It is thought to play a key role in cardiovascular homeostasis. Helps restore the body's salt and water balance. Improves heart function.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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DR EMBL; AF037466; AAB92565.1; -; Genomic_DNA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 129 Gamma-brain natriuretic peptide.
FT PEPTIDE 101 129 Brain natriuretic peptide 29 (By similarity).
FT PEPTIDE 104 129 Brain natriuretic peptide 26 (By similarity).
FT DISULFID 107 123 By similarity.
SQ SEQUENCE 129 AA; 14118 MW; 13D4DF91D32A28EF CRC64;

Query Match 80.9%; Score 55; DB 1; Length 129;
Best Local Similarity 58.8%; Pred. No. 0.00088;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 107 CFGRRLDRIKSGSLGC 123

RESULT 49

ANFC_RANCA STANDARD; PRT; 129 AA.
ID ANFC_RANCA
AC P20968;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-1 precursor (CNP I).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana; Aquarana.
OC NCBI_TaxID=8400;
OX NCBI_TaxID=8400;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94230409; PubMed=8175740;
RA Kojima M., Ohyama Y., Miyamoto K., Minamino N., Kangawa K., Matsuo H.;
RT "Cloning and characterization of a novel natriuretic peptide in frog (Rana catesbeiana).";
RL J. Biol. Chem. 269:13136-13140(1994).

CC -1- FUNCTION: Exhibits natriuretic and vasodepressor activity. Has a CGMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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DR EMBL; D17413; BAA04235.1; -; mRNA.
DR PIR; A36399; A36399.
DR PIR; A54119; A54119.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 24 Potential.
FT PROPEP 25 105
FT PEPTIDE 108 129 C-type natriuretic peptide-1.
FT DISULFID 113 129
SQ SEQUENCE 129 AA; 14656 MW; 47E0E78E32F07307 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 129;
Best Local Similarity 58.8%; Pred. No. 0.00088;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 113 CFGVKLDRIKSGSLGC 129

RESULT 50
ANFC2_FUGRU STANDARD; PRT; 130 AA.
ID ANFC2_FUGRU
AC Q805D5;
DT 25-OCT-2004 (Rel. 45, Created)

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DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-2 precursor.
GN Name=cnp-2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takei Y.;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC cGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB089936; BAC57072.1; -; mRNA.
DR Ensembl; SINFRUG00000157592; Fugu rubripes.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 101 By similarity.
FT PEPTIDE 104 130 C-type natriuretic peptide-2.
FT DISULFID 114 130 By similarity.
SQ SEQUENCE 130 AA; 13792 MW; 41BE1FC1A5F7E4C CRC64;
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Query Match 80.9%; Score 55; DB 1; Length 130;
Best Local Similarity 58.8%; Pred. No. 0.00088;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 114 CFGMKIDRIGISGLGC 130

Search completed: January 26, 2006, 14:45:17
Job time : 91 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:40:37 ; Search time 23 Seconds
 (without alignments)
 61.108 Million cell updates/sec

Title: US-10-664-605-5
 Perfect score: 68
 Sequence: 1 CFGXXXDRIGXXSXGC 17

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued Patents AA:*
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 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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265	55	80.9	151	2	US-09-428-929-5	Sequence 5, Appli	338	48	70.6	38	2	US-09-466-268B-10	Sequence 10, Appl
266	55	80.9	151	6	5212286-2	Patent No. 5212286	339	48	70.6	38	2	US-10-106-806-10	Sequence 10, Appl
267	55	80.9	152	2	US-08-916-043-2	Sequence 2, Appli	340	47	69.1	27	1	US-07-828-450-30	Sequence 30, Appl
268	55	80.9	152	2	US-09-428-929-2	Sequence 2, Appli	341	47	69.1	28	1	US-08-451-240-6	Sequence 6, Appli
269	55	80.9	152	6	5212286-6	Patent No. 5223425-11	342	47	69.1	28	1	US-08-470-846A-6	Sequence 6, Appli
270	55	80.9	241	6	5223425-11	Patent No. 5223425	343	47	69.1	28	1	US-08-470-846A-24	Sequence 24, Appl
271	54	79.4	23	6	5212286-48	Patent No. 5212286	344	47	69.1	28	2	US-08-954-915A-52	Sequence 52, Appl
272	54	79.4	25	6	5212286-36	Patent No. 5212286	345	47	69.1	28	2	US-09-154-390-6	Sequence 6, Appli
273	52	76.5	18	6	5212286-42	Patent No. 5212286	346	47	69.1	28	4	PCT-US94-12591-6	Sequence 24, Appl
274	51	75.0	32	2	US-08-954-915A-17	Sequence 17, Appl	347	47	69.1	28	4	PCT-US94-12591-6	Sequence 6, Appli
275	50	73.5	26	1	US-08-850-910A-1	Sequence 1, Appli	348	47	69.1	32	1	US-08-451-240-5	Sequence 5, Appli
276	50	73.5	26	2	US-10-106-806-7	Sequence 7, Appli	349	47	69.1	32	1	US-08-470-846A-5	Sequence 5, Appli
277	50	73.5	26	2	US-09-902-517-1	Sequence 1, Appli	350	47	69.1	32	2	US-09-154-390-5	Sequence 5, Appli
278	50	73.5	32	1	US-07-828-450-41	Sequence 41, Appl	351	47	69.1	32	4	PCT-US94-12591-5	Sequence 5, Appli
279	50	73.5	32	1	US-08-297-330-2	Sequence 2, Appli	352	46	67.6	17	1	US-07-828-450-19	Sequence 19, Appl
280	50	73.5	32	1	US-08-451-240-3	Sequence 3, Appli	353	46	67.6	21	1	US-07-781-590A-15	Sequence 15, Appl
281	50	73.5	32	1	US-08-451-240-22	Sequence 22, Appl	354	46	67.6	21	2	US-09-466-268B-8	Sequence 8, Appli
282	50	73.5	32	1	US-08-470-846A-3	Sequence 3, Appli	355	46	67.6	28	1	US-08-451-240-25	Sequence 25, Appl
283	50	73.5	32	2	US-08-954-915A-21	Sequence 21, Appl	356	46	67.6	28	1	US-08-470-846A-27	Sequence 27, Appl
284	50	73.5	32	2	US-08-954-915A-23	Sequence 23, Appl	357	46	67.6	28	2	US-08-954-915A-50	Sequence 50, Appl
285	50	73.5	32	2	US-08-954-915A-48	Sequence 48, Appl	358	46	67.6	28	2	US-09-154-390-27	Sequence 27, Appl
286	50	73.5	32	2	US-08-942-332B-1	Sequence 1, Appli	359	46	67.6	28	4	PCT-US94-12591-25	Sequence 25, Appl
287	50	73.5	32	2	US-08-942-456-1	Sequence 1, Appli	360	46	67.6	32	2	US-08-954-915A-1	Sequence 1, Appli
288	50	73.5	32	2	US-09-510-721-1	Sequence 1, Appli	361	45.5	66.9	27	6	5204327-2	Patent No. 5204327
289	50	73.5	32	2	US-09-466-268B-6	Sequence 6, Appli	362	45	66.2	20	1	US-08-257-446-3	Sequence 3, Appli
290	50	73.5	32	2	US-09-154-390-3	Sequence 3, Appli	363	44	64.7	32	2	US-08-954-915A-4	Sequence 4, Appli
291	50	73.5	32	2	US-09-154-390-22	Sequence 22, Appl	364	44	64.7	32	2	US-08-954-915A-11	Sequence 11, Appl
292	50	73.5	32	2	US-10-106-806-6	Sequence 6, Appli	365	44	64.7	32	2	US-08-954-915A-12	Sequence 12, Appl
293	50	73.5	32	2	US-09-623-548A-509	Sequence 509, App	366	44	64.7	32	2	US-08-954-915A-14	Sequence 14, Appl
294	50	73.5	32	2	US-09-623-548A-516	Sequence 516, App	367	44	64.7	32	2	US-08-954-915A-24	Sequence 24, Appl
295	50	73.5	32	2	US-09-657-276-509	Sequence 509, App	368	44	64.7	32	2	US-08-954-915A-43	Sequence 43, Appl
296	50	73.5	32	2	US-09-657-276-516	Sequence 516, App	369	43	63.2	32	2	US-08-954-915A-5	Sequence 5, Appli
297	50	73.5	32	2	US-09-902-517-49	Sequence 49, Appl	370	43	63.2	32	2	US-08-954-915A-15	Sequence 15, Appl
298	50	73.5	32	4	PCT-US94-02391-2	Sequence 2, Appli	371	43	63.2	32	2	US-08-954-915A-16	Sequence 16, Appl
299	50	73.5	32	4	PCT-US94-12591-3	Sequence 3, Appli	372	43	63.2	32	2	US-08-954-915A-19	Sequence 19, Appl
300	50	73.5	33	2	US-09-942-709-1	Sequence 22, Appli	373	43	63.2	32	2	US-08-954-915A-22	Sequence 22, Appl
301	50	73.5	35	2	US-09-623-548A-506	Sequence 506, App	374	42	61.8	32	2	US-08-954-915A-6	Sequence 6, Appli
302	50	73.5	35	2	US-09-623-548A-506	Sequence 506, App	375	42	61.8	32	2	US-08-954-915A-13	Sequence 13, Appl
303	50	73.5	35	2	US-09-657-276-506	Sequence 506, App	376	42	61.8	32	2	US-08-954-915A-18	Sequence 18, Appl
304	50	73.5	41	2	US-09-466-268B-1	Sequence 1, Appli	377	42	61.8	32	2	US-08-954-915A-26	Sequence 26, Appl
305	50	73.5	41	2	US-10-106-806-1	Sequence 1, Appli	378	41	60.3	25	2	US-09-466-268B-7	Sequence 7, Appli
306	50	73.5	134	1	US-08-850-910A-45	Sequence 45, Appl	379	41	60.3	28	1	US-08-451-240-10	Sequence 10, Appl
307	50	73.5	134	1	US-08-850-910A-48	Sequence 48, Appl	380	41	60.3	28	1	US-08-470-846A-10	Sequence 10, Appl
308	50	73.5	134	2	US-09-508-435A-2	Sequence 2, Appli	381	41	60.3	28	2	US-09-154-390-10	Sequence 10, Appl
309	50	73.5	134	2	US-09-902-517-45	Sequence 45, Appl	382	41	60.3	28	4	PCT-US94-12591-10	Sequence 10, Appl
310	50	73.5	134	2	US-09-902-517-48	Sequence 48, Appl	383	41	60.3	2	2	US-10-360-101-86	Sequence 86, Appl
311	49	72.1	20	6	5212286-54	Patent No. 5212286	384	40	58.8	17	1	US-07-828-450-20	Sequence 20, Appl
312	49	72.1	20	6	5212286-58	Patent No. 5212286	385	40	58.8	20	1	US-08-257-446-4	Sequence 4, Appli
313	49	72.1	23	6	5212286-44	Patent No. 5212286	386	40	58.8	21	2	US-09-623-548A-496	Sequence 496, App
314	49	72.1	23	6	5212286-45	Patent No. 5212286	387	40	58.8	21	2	US-09-657-276-496	Sequence 496, App
315	49	72.1	23	6	5212286-53	Patent No. 5212286	388	40	58.8	22	1	US-07-781-590A-17	Sequence 17, Appl
316	49	72.1	24	6	5212286-52	Patent No. 5212286	389	40	58.8	25	6	5212286-49	Patent No. 5212286
317	49	72.1	24	6	5212286-56	Patent No. 5212286	390	40	58.8	28	1	US-08-451-240-11	Sequence 11, Appl
318	49	72.1	25	6	5212286-32	Patent No. 5212286	391	40	58.8	28	1	US-08-451-240-23	Sequence 23, Appl
319	49	72.1	25	6	5212286-33	Patent No. 5212286	392	40	58.8	28	1	US-08-451-240-34	Sequence 34, Appl

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395	40	58.8	28	1	US-08-470-846A-25	Sequence 25, Appl
396	40	58.8	28	1	US-08-470-846A-31	Sequence 31, Appl
397	40	58.8	28	1	US-08-470-846A-32	Sequence 32, Appl
398	40	58.8	28	2	US-09-154-390-11	Sequence 11, Appl
399	40	58.8	28	2	US-09-154-390-19	Sequence 19, Appl
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402	40	58.8	28	4	PCT-US94-12591-11	Sequence 11, Appl
403	40	58.8	28	4	PCT-US94-12591-23	Sequence 23, Appl
404	40	58.8	28	4	PCT-US94-12591-34	Sequence 34, Appl
405	40	58.8	32	1	US-08-451-240-15	Sequence 15, Appl
406	40	58.8	32	1	US-08-470-846A-15	Sequence 15, Appl
407	40	58.8	32	2	US-08-954-915A-20	Sequence 20, Appl
408	40	58.8	32	2	US-09-154-390-15	Sequence 15, Appl
409	40	58.8	32	4	PCT-US94-12591-15	Sequence 15, Appl
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412	39	57.4	13	6	5212286-46	Patent No. 5212286
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414	39	57.4	15	2	US-09-657-276-493	Sequence 493, App
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417	39	57.4	28	1	US-08-451-240-13	Sequence 13, Appl
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422	39	57.4	28	2	US-09-154-390-12	Sequence 12, Appl
423	39	57.4	28	2	US-09-154-390-13	Sequence 13, Appl
424	39	57.4	28	2	US-09-154-390-26	Sequence 26, Appl
425	39	57.4	28	4	PCT-US94-12591-12	Sequence 12, Appl
426	39	57.4	28	4	PCT-US94-12591-13	Sequence 13, Appl
427	39	57.4	28	4	PCT-US94-12591-24	Sequence 24, Appl
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433	37	54.4	15	6	5212286-24	Patent No. 5212286
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436	37	54.4	22	1	US-07-828-450-21	Sequence 21, Appl
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443	37	54.4	32	2	US-08-954-915A-28	Sequence 28, Appl
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454	34	50.0	28	4	PCT-US94-12591-36	Sequence 36, Appl
455	34	50.0	28	4	PCT-US94-12591-37	Sequence 37, Appl
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462	33	48.5	28	1	US-08-451-240-36	Sequence 36, Appl
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465	33	48.5	28	2	US-09-154-390-34	Sequence 34, Appl

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469	33	48.5	28	4	PCT-US94-12591-32	Sequence 32, Appl
470	33	48.5	28	4	PCT-US94-12591-35	Sequence 35, Appl
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490	31	45.6	28	1	US-08-451-240-31	Sequence 31, Appl
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493	31	45.6	28	2	US-09-154-390-33	Sequence 33, Appl
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495	31	45.6	28	4	PCT-US94-12591-31	Sequence 31, Appl
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507	31	45.6	480	2	US-09-489-039A-13045	Sequence 13045, A
508	31	45.6	569	2	US-09-252-991A-29263	Sequence 29263, A
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515	30	44.1	148	2	US-09-252-991A-21985	Sequence 21985, A
516	30	44.1	153	2	US-09-902-540-11201	Sequence 11201, A
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519	30	44.1	181	2	US-08-828-683A-1	Sequence 1, Appli
520	30	44.1	255	2	US-09-949-016-8309	Sequence 8309, Ap
521	30	44.1	294	2	US-09-270-767-59588	Sequence 59588, A
522	30	44.1	392	2	US-09-902-540-13511	Sequence 13511, A
523	30	44.1	402	2	US-09-489-039A-10525	Sequence 10525, A
524	30	44.1	405	2	US-09-543-681A-4311	Sequence 4311, Ap
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526	30	44.1	415	2	US-09-134-000C-4092	Sequence 4092, Ap
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529	30	44.1	417	2	US-09-565-918-5	Sequence 5, Appli
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535	30	44.1	417	2	US-09-565-009B-5	Sequence 5, Appli
536	30	44.1	417	2	US-10-175-902-5	Sequence 5, Appli
537	30	44.1	417	2	US-09-314-889-4	Sequence 4, Appli
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540	30	44.1	428	2	US-09-557-908-2	Sequence 2, Appli	613	28	41.2	90	1	US-08-308-086-6	Sequence 6, Appli
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543	30	44.1	430	2	US-09-252-991A-22599	Sequence 22599, A	616	28	41.2	92	1	US-08-479-078-18	Sequence 18, Appli
544	30	44.1	444	2	US-09-328-352-5249	Sequence 5249, Ap	617	28	41.2	92	1	US-08-805-445-21	Sequence 21, Appli
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546	30	44.1	474	2	US-09-489-039A-8680	Sequence 8680, Ap	619	28	41.2	92	1	US-09-066-208-21	Sequence 21, Appli
547	30	44.1	513	2	US-09-252-991A-22040	Sequence 22040, A	620	28	41.2	94	1	US-08-167-035-23	Sequence 23, Appli
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549	30	44.1	585	2	US-09-248-796A-20176	Sequence 20176, A	622	28	41.2	94	1	US-08-539-005-23	Sequence 23, Appli
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559	30	44.1	2544	2	US-09-436-063C-3	Sequence 3, Appli	632	28	41.2	217	2	US-09-724-623-112	Sequence 112, App
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571	29	42.6	29	4	PCT-US94-12591-18	Sequence 18, Appli	644	28	41.2	381	2	US-09-252-991A-26281	Sequence 26281, A
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594	29	42.6	462	2	US-09-328-352-4819	Sequence 4819, Ap	665	28	41.2	819	2	US-09-651-656-15	Sequence 15, Appli
595	29	42.6	514	2	US-09-602-787A-502	Sequence 502, App	666	28	41.2	819	2	US-09-650-855-15	Sequence 15, Appli
596	29	42.6	540	2	US-09-469-211A-3	Sequence 3, Appli	667	28	41.2	827	2	US-09-252-991A-24033	Sequence 24033, A
597	29	42.6	540	2	US-09-902-540-11379	Sequence 11379, A	668	28	41.2	870	1	US-08-190-687B-25	Sequence 25, Appli
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599	29	42.6	545	2	US-09-252-991A-29078	Sequence 29078, A	670	28	41.2	880	2	US-09-538-092-577	Sequence 577, App
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606	29	42.6	817	1	US-09-538-092-739	Sequence 739, App	677	28	41.2	3122	2	US-09-198-452A-230	Sequence 230, App
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			48	2	US-09-270-767-38501	Sequence 38501, A	684	27	39.7	73	2	US-09-513-999C-7202	Sequence 7202, Ap
			48	2	US-09-270-767-53718	Sequence 53718, A				92	2	US-09-489-039A-13903	Sequence 13903, A

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691	27	39.7	127	1	US-08-473-503-45	Sequence 45, Appl
692	27	39.7	127	1	US-08-483-932-45	Sequence 45, Appl
693	27	39.7	127	1	US-08-720-420A-45	Sequence 45, Appl
694	27	39.7	127	2	US-08-714-017-45	Sequence 45, Appl
695	27	39.7	127	2	US-08-475-680-45	Sequence 45, Appl
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710	27	39.7	313	2	US-09-800-729-196	Sequence 328, App
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712	27	39.7	326	2	US-09-884-570-8	Sequence 8, Appli
713	27	39.7	326	2	US-10-157-457A-8	Sequence 4, Appli
714	27	39.7	333	2	US-09-562-737-4	Sequence 22942, A
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725	27	39.7	412	2	US-09-402-532-6	Sequence 157, App
726	27	39.7	412	2	US-09-999-833A-157	Sequence 5, Appli
727	27	39.7	412	2	US-10-020-445A-157	Sequence 9364, Ap
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732	27	39.7	425	2	US-09-711-164-428	Sequence 7, Appli
733	27	39.7	433	2	US-09-328-352-6503	Sequence 6293, Ap
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749	27	39.7	547	2	US-09-949-016-7043	Sequence 14001, A
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757	27	39.7	1461	2	US-10-142-231-86	

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759	27	39.7	1497	2	US-09-529-904-3	Sequence 3, Appli
760	27	39.7	1747	2	US-09-949-016-7835	Sequence 7835, Ap
761	27	39.7	1927	2	US-09-949-016-6206	Sequence 6206, Ap
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763	27	39.7	2710	1	US-08-487-826B-12	Sequence 12, Appl
764	27	39.7	2710	2	US-09-210-288-12	Sequence 12, Appl
765	27	39.7	2710	2	US-10-153-273-12	Sequence 12, Appl
766	27	39.7	3060	1	US-08-487-826B-14	Sequence 14, Appl
767	27	39.7	3907	2	US-10-029-217A-24	Sequence 24, Appl
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769	26.5	39.0	212	2	US-09-216-066-1	Sequence 1, Appli
770	26.5	39.0	477	2	US-09-118-324-2	Sequence 2, Appli
771	26.5	39.0	485	1	US-08-453-956-15	Sequence 15, Appl
772	26.5	39.0	485	1	US-08-086-631-15	Sequence 15, Appl
773	26.5	39.0	485	1	US-08-452-930-15	Sequence 15, Appl
774	26.5	39.0	485	2	US-10-010-065-2	Sequence 2, Appli
775	26.5	39.0	485	4	PCT-US93-08174-15	Sequence 15, Appl
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779	26	38.2	54	2	US-09-270-767-61307	Sequence 61307, A
780	26	38.2	54	2	US-08-563-148E-1	Sequence 1, Appli
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783	26	38.2	70	1	US-08-009-265-30	Sequence 30, Appl
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786	26	38.2	70	1	US-08-682-485A-22	Sequence 22, Appl
787	26	38.2	70	1	US-08-682-485A-23	Sequence 23, Appl
788	26	38.2	70	1	US-08-451-472-42	Sequence 42, Appl
789	26	38.2	70	1	US-08-933-314-21	Sequence 21, Appl
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791	26	38.2	70	1	US-08-933-314-23	Sequence 23, Appl
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793	26	38.2	71	2	US-08-472-053-45	Sequence 48, Appl
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797	26	38.2	84	2	US-08-882-431B-18	Sequence 18, Appl
798	26	38.2	84	2	US-09-270-767-36752	Sequence 36752, A
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806	26	38.2	94	1	US-08-454-730-6	Sequence 6, Appli
807	26	38.2	94	2	US-08-949-788-6	Sequence 6, Appli
808	26	38.2	95	2	US-09-621-976-4670	Sequence 4670, Ap
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830	26	38.2	151	1	US-08-563-148E-6	Sequence 6, Appli

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864	26	38.2	236	2	US-09-216-430C-14	Sequence 14, Appli	937	26	38.2	468	2	US-09-004-838-121	Sequence 121, App
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875	26	38.2	255	2	US-09-877-338-2	Sequence 8, Appli	948	26	38.2	539	2	US-09-173-281-20	Sequence 20, Appli
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983 26 38.2 1106 2 US-09-949-016-9626 Sequence 9626, Ap
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995 26 38.2 1172 2 US-09-919-172-16 Sequence 16, Appl
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997 26 38.2 1180 2 US-09-543-681A-6436 Sequence 6436, Ap
998 26 38.2 1186 2 US-09-560-385A-18 Sequence 18, Appl
999 26 38.2 1404 2 US-09-345-473E-24 Sequence 24, Appl
1000 26 38.2 1404 2 US-09-862-027-24 Sequence 24, Appl
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ALIGNMENTS

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RESULT 1
US-09-579-883A-13
; Sequence 13, Application US/09579883A
; Patent No. 6686443
; GENERAL INFORMATION:
; APPLICANT: RABENSTEIN, DALLAS
; APPLICANT: SHI, TIESHENG
; TITLE OF INVENTION: CHEMICAL REAGENTS FOR FORMATION OF DISULFIDE BONDS IN PEPTIDES
; FILE REFERENCE: 407T-891100US
; CURRENT APPLICATION NUMBER: US/09/579,883A
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-579-883A-13

Query Match          82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 4.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db      1 CFGSRIDRIGAQSGMGC 17

RESULT 2
US-09-623-548A-469
; Sequence 469, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
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; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 469
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-469
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Query Match          82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 4.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Db      1 CFGSRIDRIGAQSGMGC 17
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RESULT 3
US-09-657-276-469
; Sequence 469, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 469
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-469

Query Match          82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 4.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXXRIGXXSXXGC 17
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Db      1 CFGSRIDRIGAQSGMGC 17

RESULT 4
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US-09-623-548A-470
; Sequence 470, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 470
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-623-548A-470

Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 4.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 1 CFGSRIDRIGAQSGMGC 17

RESULT 5
US-09-657-276-470
; Sequence 470, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 470
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide
US-09-657-276-470

Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 4.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 1 CFGSRIDRIGAQSGMGC 17

RESULT 6
5212286-43
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:43
; LENGTH: 23
5212286-43

Query Match 82.4%; Score 56; DB 6; Length 23;
Best Local Similarity 58.8%; Pred. No. 5.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 2 CFGGRIDRIGAQSALGC 18

RESULT 7
5212286-47
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
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5212286-47

Query Match 82.4%; Score 56; DB 6; Length 23;
Best Local Similarity 58.8%; Pred. No. 5.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 2 CFGARIDRIGAQSGLC 18

RESULT 8

US-07-754-958-4
; Sequence 4, Application US/07754958
; Patent No. 5336759
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOTO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,958
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 56281
; REFERENCE/DOCKET NUMBER: 9437/92322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-754-958-4

Query Match 82.4%; Score 56; DB 1; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 9
US-07-754-947-4
; Sequence 4, Application US/07754947
; Patent No. 5338830
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOTO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,947
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 5683/92321
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-754-947-4

Query Match 82.4%; Score 56; DB 1; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 10
US-09-623-548A-468
; Sequence 468, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 468
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-623-548A-468

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
Db 4 CFGSRIDRIGAQSGMGC 20


```

RESULT 11
US-09-623-548A-471
; Sequence 471, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 471
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;
US-09-623-548A-471
  
```

```

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
  
```

```

QY      1 CFGXXXDRIGXXSXGC 17
Db      4 CFGSRIDRIGAQSGMGC 20
  
```

```

RESULT 12
US-09-657-276-468
; Sequence 468, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 468
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
  
```

```

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-468
  
```

```

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
  
```

```

QY      1 CFGXXXDRIGXXSXGC 17
Db      4 CFGSRIDRIGAQSGMGC 20
  
```

```

RESULT 13
US-09-657-276-471
; Sequence 471, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 471
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-471
  
```

```

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
  
```

```

QY      1 CFGXXXDRIGXXSXGC 17
Db      4 CFGSRIDRIGAQSGMGC 20
  
```

```

RESULT 14
5212286-31
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
  
```

```
;SEQ ID NO:31:
;   LENGTH: 25
5212286-31

Query Match      82.4%; Score 56; DB 6; Length 25;
Best Local Similarity 58.8%; Pred. No. 5.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      4 CFGGRIDRIGAQSALGC 20

RESULT 15
5212286-35
;Patent No. 5212286
;APPLICANT: LEWICKI, JOHN A.;SCARBOROUGH, ROBERT M.
;TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
;PEPTIDE COMPUnds
;   NUMBER OF SEQUENCES: 68
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/870,795
;   FILING DATE: 05-JUN-1986
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 766,030
;   FILING DATE: 08-MAY-1985
;   APPLICATION NUMBER: 602,117
;   FILING DATE: 09-APR-1984
;   APPLICATION NUMBER: 616,488
;   FILING DATE: 01-JUN-1984
;SEQ ID NO:35:
;   LENGTH: 25
5212286-35

Query Match      82.4%; Score 56; DB 6; Length 25;
Best Local Similarity 58.8%; Pred. No. 5.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      4 CFGARIDRIGAQSGLGC 20

RESULT 16
US-08-451-240-14
;Sequence 14, Application US/08451240
;Patent No. 5665704
;GENERAL INFORMATION:
;APPLICANT: Lowe, David
;APPLICANT: Cunningham, Brian
;APPLICANT: Oare, David
;APPLICANT: McDowell, Robert S.
;APPLICANT: Burnier, John
;TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
;TITLE OF INVENTION: PEPTIDES
;NUMBER OF SEQUENCES: 47
;CORRESPONDENCE ADDRESS:
;ADDRESSEE: Genentech, Inc.
;STREET: 460 Point San Bruno Blvd
;CITY: South San Francisco
;STATE: California
;COUNTRY: USA
;ZIP: 94080
;COMPUTER READABLE FORM:
;MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;COMPUTER: IBM PC compatible
;OPERATING SYSTEM: PC-DOS/MS-DOS
;SOFTWARE: patin (Genentech)
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/451,240
;FILING DATE:
;CLASSIFICATION: 530
;PRIOR APPLICATION DATA:
```

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;APPLICATION NUMBER: 08/362552
;FILING DATE: 06-JAN-1995
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 08/152994
;FILING DATE: 12-NOV-1993
;ATTORNEY/AGENT INFORMATION:
;NAME: Kubinec, Jeffrey S.
;REGISTRATION NUMBER: 36,575
;REFERENCE/DOCKET NUMBER: P0844P1C1
;TELECOMMUNICATION INFORMATION:
;TELEPHONE: 415/225-8228
;TELEFAX: 415/952-9881
;TELEX: 910/371-7168
;INFORMATION FOR SEQ ID NO: 14:
;SEQUENCE CHARACTERISTICS:
;LENGTH: 28 amino acids
;TYPE: amino acid
;TOPOLOGY: linear
US-08-451-240-14

Query Match      82.4%; Score 56; DB 1; Length 28;
Best Local Similarity 58.8%; Pred. No. 6.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      7 CFGKSMDRIGAQSGLGC 23

RESULT 17
US-08-470-846A-14
;Sequence 14, Application US/08470846A
;Patent No. 5846932
;GENERAL INFORMATION:
;APPLICANT: Genentech, Inc.
;APPLICANT: Lowe, David G.
;APPLICANT: Cunningham, Brian C.
;APPLICANT: Oare, David
;APPLICANT: McDowell, Robert S.
;APPLICANT: Burnier, John
;TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
;NUMBER OF SEQUENCES: 43
;CORRESPONDENCE ADDRESS:
;ADDRESSEE: Genentech, Inc.
;STREET: 460 Point San Bruno Blvd
;CITY: South San Francisco
;STATE: California
;COUNTRY: USA
;ZIP: 94080
;COMPUTER READABLE FORM:
;MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;COMPUTER: IBM PC compatible
;OPERATING SYSTEM: PC-DOS/MS-DOS
;SOFTWARE: winpatin (Genentech)
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/470,846A
;FILING DATE: 06-Jun-1995
;CLASSIFICATION: 514
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 08/419877
;FILING DATE: 11-APR-1995
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 08/362552
;FILING DATE: 06-JAN-1995
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 08/152994
;FILING DATE: 12-NOV-1993
;ATTORNEY/AGENT INFORMATION:
;NAME: Kubinec, Jeffrey S.
;REGISTRATION NUMBER: 36,575
;REFERENCE/DOCKET NUMBER: P0844P2C1
;TELECOMMUNICATION INFORMATION:
;TELEPHONE: 415/225-8228
```

TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-470-846A-14

Query Match 82.4%; Score 56; DB 1; Length 28;
Best Local Similarity 58.8%; Pred. No. 6.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGXC 17
||| ||| | ||
Db 7 CFGKSMDRIGAQSGLGC 23

RESULT 18

US-09-154-390-14
Sequence 14, Application US/09154390
Patent No. 6525022
GENERAL INFORMATION:
APPLICANT: Lowe, David G.
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John P.
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
FILE REFERENCE: 13734.1USWS
CURRENT APPLICATION NUMBER: US/09/154,390
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: US 08/470,846
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/419,877
PRIOR FILING DATE: 1995-04-11
PRIOR APPLICATION NUMBER: US 08/362,552
PRIOR FILING DATE: 1995-01-06
PRIOR APPLICATION NUMBER: PCT/US94/12591
PRIOR FILING DATE: 1994-11-04
PRIOR APPLICATION NUMBER: US 08/152,994
PRIOR FILING DATE: 1993-11-12
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-154-390-14

Query Match 82.4%; Score 56; DB 2; Length 28;
Best Local Similarity 58.8%; Pred. No. 6.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGXC 17
||| ||| | ||
Db 7 CFGKSMDRIGAQSGLGC 23

RESULT 19

PCT-US94-12591-14
Sequence 14, Application PC/TUS9412591
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
PEPTIDES

NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/152994

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Daryl B.

REGISTRATION NUMBER: 32,637

REFERENCE/DOCKET NUMBER: 844P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1249

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US94-12591-14

Query Match 82.4%; Score 56; DB 4; Length 28;
Best Local Similarity 58.8%; Pred. No. 6.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGXC 17
||| ||| | ||
Db 7 CFGKSMDRIGAQSGLGC 23

RESULT 20

US-09-623-548A-472
Sequence 472, Application US/09623548A
Patent No. 6849714
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/623,548A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 472
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence


```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-472

```

```

Query Match      82.4%; Score 56; DB 2; Length 30;
Best Local Similarity 58.8%; Pred. No. 7e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      11 CFGSRIDRIGAGSGMGC 27

```

```

RESULT 21
US-09-657-276-472
; Sequence 472, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 472
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-472

```

```

Query Match      82.4%; Score 56; DB 2; Length 30;
Best Local Similarity 58.8%; Pred. No. 7e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      11 CFGSRIDRIGAGSGMGC 27

```

```

RESULT 22
US-07-828-450-7
; Sequence 7, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIHARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
;

```

```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-828-450-7

```

```

Query Match      80.9%; Score 55; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      1 CFGKLDRIGSMGLGC 17

```

```

RESULT 23
US-08-737-927-1
; Sequence 1, Application US/08737927
; Patent No. 5767239
; GENERAL INFORMATION:
; APPLICANT: IMMER, Hansueli
; APPLICANT: FORSMANN, Wolf-Georg
; APPLICANT: ADERMAN, Knut
; APPLICANT: KLESSEN, Christian
; TITLE OF INVENTION: PROCESS AND INTERMEDIATE PRODUCTS FOR
; TITLE OF INVENTION: PREPARING CARDIODILATIN FRAGMENTS, AND HIGHLY PURIFIED
; TITLE OF INVENTION: CARDIODILATIN FRAGMENTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,927
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/33769
; FILING DATE: 14-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kltts, Monica C.
; REGISTRATION NUMBER: 36,105
;

```

```
; REFERENCE/DOCKET NUMBER: P1614-6052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-737-927-1

Query Match      80.9%; Score 55; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXXGC 17
        ||| ||| ||| |||
Db      1 CFGGRMDRIGAGSGLGC 17

RESULT 24
US-08-850-910A-15
; Sequence 15, Application US/08850910A
; Patent No. 5948761
; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J.J.
; APPLICANT: LEWICKI, J.
; APPLICANT: SCARBOROUGH, R.M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
; APPLICATION NUMBER: 07/299,880
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 07/206,470
; FILING DATE: 14-JUN-1988
; APPLICATION NUMBER: 07/200,383
; FILING DATE: 31-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 219002025212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

```
US-08-850-910A-15

Query Match      80.9%; Score 55; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXXGC 17
        ||| ||| ||| |||
Db      1 CFGRRLDRIIGSLGLGC 17

RESULT 25
US-09-623-548A-474
; Sequence 474, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 474
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-623-548A-474

Query Match      80.9%; Score 55; DB 2; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXXGC 17
        ||| ||| ||| |||
Db      1 CFGGRMDRIGAGSGLGC 17

RESULT 26
US-09-657-276-474
; Sequence 474, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
```

```

; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 474
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-474

```

```

Query Match      80.9%; Score 55; DB 2; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      1 CFGRMDRIGAQSGLGC 17

```

```

RESULT 27
US-09-902-517-15
; Sequence 15, Application US/09902517
; Patent No. 6897030
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Proviso formula (1)
US-09-902-517-15

```

```

Query Match      80.9%; Score 55; DB 2; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      1 CFGRDLRIGSLGLGC 17

```

```

RESULT 28
US-08-850-910A-32
; Sequence 32, Application US/08850910A
; Patent No. 5948761

```

```

; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J.J.
; APPLICANT: LEWICKI, J.
; APPLICANT: SCARBOROUGH, R.M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
; APPLICATION NUMBER: 07/299,880
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 07/206,470
; FILING DATE: 14-JUN-1988
; APPLICATION NUMBER: 07/200,383
; FILING DATE: 31-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 219002025212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
US-08-850-910A-32

```

```

Query Match      80.9%; Score 55; DB 1; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy      1 CFGXXXDRIGXXSXGC 17
      ||| ||||| | ||
Db      3 CFGRMDRIGAQSGLGC 19

```

```

RESULT 29
US-08-850-910A-34
; Sequence 34, Application US/08850910A
; Patent No. 5948761
; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J.J.
; APPLICANT: LEWICKI, J.
; APPLICANT: SCARBOROUGH, R.M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington

```



```
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
; APPLICATION NUMBER: 07/299,880
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 07/206,470
; FILING DATE: 14-JUN-1988
; APPLICATION NUMBER: 07/200,383
; FILING DATE: 31-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 219002025212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-850-910A-34

Query Match      80.9%; Score 55; DB 1; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      3 CFGRRLDRIQSLGSLGC 19

RESULT 30
US-09-902-517-32
; Sequence 32, Application US/09902517
; Patent No. 6897030
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
```

```
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amino acids encoding pBNP
; US-09-902-517-32

Query Match      80.9%; Score 55; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      3 CFGRMDRIGAQSGLGC 19

RESULT 31
US-09-902-517-34
; Sequence 34, Application US/09902517
; Patent No. 6897030
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amino acids encoding pBNP
; US-09-902-517-34

Query Match      80.9%; Score 55; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      3 CFGRRLDRIQSLGSLGC 19

RESULT 32
5212286-30
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
```

```

; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:30:
; LENGTH: 20
5212286-30

Query Match      80.9%; Score 55; DB 6; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy      1 CFGXXXDRIGXXSXGC 17
      ||| |||| | ||
Db      4 CFGGRMDRIGAQSGLGC 20

RESULT 33
5212286-51
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:51:
; LENGTH: 20
5212286-51

Query Match      80.9%; Score 55; DB 6; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy      1 CFGXXXDRIGXXSXGC 17
      ||| |||| | ||
Db      4 CFGRRIDRIGAQSGLGC 20

RESULT 34
US-08-257-446-2
; Sequence 2, Application US/08257446
; Patent No. 5565606
; GENERAL INFORMATION:
; APPLICANT: Briephol, Gerhard
; APPLICANT: Knolle, Jochem
; TITLE OF INVENTION: The Synthesis of Peptide
; TITLE OF INVENTION: Aminoalkylamides and Peptide Hydrazides by the solid phase
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,446
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 783,335
; FILING DATE: 28-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lindeman, Jeffrey A.
; REGISTRATION NUMBER: 34,658
; REFERENCE/DOCKET NUMBER: 02481-0503-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-208-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-257-446-2

Query Match      80.9%; Score 55; DB 1; Length 21;
Best Local Similarity 58.8%; Pred. No. 7.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy      1 CFGXXXDRIGXXSXGC 17
      ||| |||| | ||
Db      2 CFGGRIDRIGAQSGLGC 18
```

```

RESULT 35
US-09-623-548A-483
; Sequence 483, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 483
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-483
```

```

Query Match      80.9%; Score 55; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 7.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy      1 CFGXXXDRIGXXSXGC 17
      ||| |||| | ||
```

Db 3 CFGGRIDRIGAGSLGC 19

RESULT 36
US-09-657-276-483
; Sequence 483, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 483
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-483

Query Match 80.9%; Score 55; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 7.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 3 CFGGRIDRIGAGSLGC 19

RESULT 37
5212286-41
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:41
; LENGTH: 21
5212286-41

Query Match 80.9%; Score 55; DB 6; Length 21;
Best Local Similarity 58.8%; Pred. No. 7.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||

Db 2 CFGGRIDRIGAGSLGC 18

RESULT 38
US-07-754-958-1
; Sequence 1, Application US/07754958
; Patent No. 5336759
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOTO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,958
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 56281
; REFERENCE/DOCKET NUMBER: 9437/92322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-754-958-1

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 6 CFGVKLDRIGAFSGLGC 22

RESULT 39
US-07-754-958-7
; Sequence 7, Application US/07754958
; Patent No. 5336759
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOTO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:


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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,958
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 56281
; REFERENCE/DOCKET NUMBER: 9437/92322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-754-958-7

```

```

Query Match      80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

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QY      1 CFGXXXXRIGXXSXGC 17
      ||| ||| | |||
Db      6 CFGKLDRIGSMGLGC 22

```

RESULT 40

```

; US-07-754-947-1
; Sequence 1, Application US/07754947
; Patent No. 5338830
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOITO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,947
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 5683/92321
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-754-947-1

```

```

Query Match      80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXXRIGXXSXGC 17
      ||| ||| | |||
Db      6 CFGVKLDRIGSMGLGC 22

```

RESULT 41

```

; US-07-754-947-7
; Sequence 7, Application US/07754947
; Patent No. 5338830
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOITO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,947
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 5683/92321
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-754-947-7

```

```

Query Match      80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXXRIGXXSXGC 17
      ||| ||| | |||
Db      6 CFGKLDRIGSMGLGC 22

```

RESULT 42

```

; US-07-728-221B-2
; Sequence 2, Application US/07728221B
; Patent No. 5340920
; GENERAL INFORMATION:
; APPLICANT: Matsuo, Hisayuki
; APPLICANT: Kangawa, Kenji
; APPLICANT: Minamino, Naoto

```

;
; TITLE OF INVENTION: NOVEL HYSIOLOGICALLY ACTIVE PORCINE
; TITLE OF INVENTION: PEPTIDE (CNP-53)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: ELEVENTH FLOOR, 1615 1 STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/728,221B
; FILING DATE: 19910712
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/9437/91817/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 671 4627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-728-221B-2

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 6 CFGKLDRIGMSGGLGC 22

RESULT 43
US-07-728-221B-11
; Sequence 11, Application US/07728221B
; Patent No. 5340920
; GENERAL INFORMATION:
; APPLICANT: Matsuo, Hisayuki
; APPLICANT: Kangawa, Kenji
; APPLICANT: Minamino, Naoto
; TITLE OF INVENTION: NOVEL HYSIOLOGICALLY ACTIVE PORCINE
; TITLE OF INVENTION: PEPTIDE (CNP-53)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: ELEVENTH FLOOR, 1615 1 STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/728,221B
; FILING DATE: 19910712
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

;
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/9437/91817/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 671 4627 CUSH
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-728-221B-11

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 6 CFGKLDRIGMSGGLGC 22

RESULT 44
US-07-778-847-3
; Sequence 3, Application US/07778847
; Patent No. 5352770
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: PORCINE DERIVED NOVEL PHYSIOLOGICALLY
; TITLE OF INVENTION: ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,847
; FILING DATE: 19921220
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/93819
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-778-847-3

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 6 CFGKLDRIGMSGGLGC 22

Db 6 CFGLKLDRI GSMGLGC 22

RESULT 45

US-07-828-450-2

; Sequence 2, Application US/07828450
; Patent No. 5434133

; GENERAL INFORMATION:

; APPLICANT: TANAKA, SHOJI

; APPLICANT: MINAMITAKE, YOSHIHARU

; APPLICANT: KITAJIMA, YASUO

; APPLICANT: FURUYA, MAYUMI

; APPLICANT: MATSUO, HISAYUKI

; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

; STREET: 1625 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/828,450

; FILING DATE: 19920131

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26,581

; REFERENCE/DOCKET NUMBER: 9437/94133

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3067

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-828-450-2

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17

Db 6 CFGLKLDRI GSMGLGC 22

RESULT 46

US-07-828-450-8

; Sequence 8, Application US/07828450
; Patent No. 5434133

; GENERAL INFORMATION:

; APPLICANT: TANAKA, SHOJI

; APPLICANT: MINAMITAKE, YOSHIHARU

; APPLICANT: KITAJIMA, YASUO

; APPLICANT: FURUYA, MAYUMI

; APPLICANT: MATSUO, HISAYUKI

; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

; STREET: 1625 L STREET, N.W.

; CITY: WASHINGTON

STATE: D.C.
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/828,450

FILING DATE: 19920131

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: SCOTT, WATSON T.

REGISTRATION NUMBER: 26,581

REFERENCE/DOCKET NUMBER: 9437/94133

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3067

TELEFAX: 202-822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-828-450-8

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17

Db 6 CFGLKLDRI GSMGLGC 22

RESULT 47

US-07-828-450-9

; Sequence 9, Application US/07828450
; Patent No. 5434133

; GENERAL INFORMATION:

; APPLICANT: TANAKA, SHOJI

; APPLICANT: MINAMITAKE, YOSHIHARU

; APPLICANT: KITAJIMA, YASUO

; APPLICANT: FURUYA, MAYUMI

; APPLICANT: MATSUO, HISAYUKI

; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

; STREET: 1625 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/828,450

; FILING DATE: 19920131

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26,581

; REFERENCE/DOCKET NUMBER: 9437/94133

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3067

; TELEFAX: 202-822-0944

TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-828-450-9

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXSXXGC 17
||| ||| | ||
DB 6 CFCGLRDRIGSMGSLGC 22

RESULT 48

US-07-828-450-10
; Sequence 10, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIHARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-828-450-10

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXSXXGC 17
||| ||| | ||
DB 6 CFCGLKMDRIGSMGSLGC 22

RESULT 49

US-07-828-450-11
; Sequence 11, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIHARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-828-450-11

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXSXXGC 17
||| ||| | ||
DB 6 CFCGLKDRIGSMGSLGC 22

RESULT 50

US-07-828-450-12
; Sequence 12, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIHARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-828-450-12

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Query Match      80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 CFGXXXXRIGXXSXGC 17
          ||| ||| | ||
Db      6 CFGKLDRIGSQSLGC 22

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Search completed: January 26, 2006, 14:46:01
 Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:42:13 ; Search time 61 Seconds
(without alignments)
116.444 Million cell updates/sec

Title: US-10-664-605-5
Perfect score: 68
Sequence: 1 CFGXXXDRIGXXSXGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	82.4	17	4	US-10-664-605-10 Sequence 10, Appl
2	56	82.4	17	4	US-10-664-605-40 Sequence 40, Appl
3	56	82.4	17	4	US-10-664-605-45 Sequence 45, Appl
4	56	82.4	17	4	US-10-664-605-58 Sequence 58, Appl
5	56	82.4	17	4	US-10-664-605-63 Sequence 63, Appl
6	56	82.4	17	4	US-10-664-605-68 Sequence 68, Appl
7	56	82.4	20	6	US-11-066-697-469 Sequence 469, App
8	56	82.4	21	6	US-11-066-697-470 Sequence 470, App
9	56	82.4	24	3	US-09-752-724-5 Sequence 5, Appl
10	56	82.4	24	6	US-11-066-697-468 Sequence 468, App
11	56	82.4	24	6	US-11-066-697-471 Sequence 471, App
12	56	82.4	30	6	US-11-066-697-472 Sequence 472, App
13	55	80.9	17	3	US-09-902-517-15 Sequence 15, Appl
14	55	80.9	17	3	US-09-027-777B-1 Sequence 1, Appl
15	55	80.9	17	4	US-10-327-514-17 Sequence 17, Appl
16	55	80.9	17	4	US-10-327-514-18 Sequence 18, Appl
17	55	80.9	17	4	US-10-327-514-19 Sequence 19, Appl
18	55	80.9	17	4	US-10-402-021-15 Sequence 15, Appl
19	55	80.9	17	4	US-10-664-605-2 Sequence 2, Appl
20	55	80.9	17	4	US-10-664-605-41 Sequence 41, Appl
21	55	80.9	17	4	US-10-664-605-42 Sequence 42, Appl
22	55	80.9	17	4	US-10-664-605-43 Sequence 43, Appl
23	55	80.9	17	4	US-10-664-605-44 Sequence 44, Appl
24	55	80.9	17	4	US-10-664-605-46 Sequence 46, Appl
25	55	80.9	17	4	US-10-664-605-47 Sequence 47, Appl
26	55	80.9	17	4	US-10-664-605-54 Sequence 54, Appl
27	55	80.9	17	4	US-10-664-605-56 Sequence 56, Appl

28	55	80.9	17	4	US-10-664-605-59 Sequence 59, Appl
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33	55	80.9	17	4	US-10-664-605-66 Sequence 66, Appl
34	55	80.9	17	4	US-10-664-605-67 Sequence 67, Appl
35	55	80.9	17	4	US-10-664-605-69 Sequence 69, Appl
36	55	80.9	17	5	US-10-499-762-17 Sequence 17, Appl
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38	55	80.9	17	5	US-10-499-762-19 Sequence 19, Appl
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42	55	80.9	20	4	US-10-402-021-32 Sequence 32, Appl
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44	55	80.9	21	6	US-11-066-697-483 Sequence 483, App
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47	55	80.9	22	3	US-09-752-724-10 Sequence 10, Appl
48	55	80.9	22	3	US-09-752-724-11 Sequence 11, Appl
49	55	80.9	22	3	US-09-466-268B-9 Sequence 9, Appl
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51	55	80.9	22	4	US-10-106-806-8 Sequence 8, Appl
52	55	80.9	22	4	US-10-106-806-9 Sequence 9, Appl
53	55	80.9	22	4	US-10-664-605-1 Sequence 1, Appl
54	55	80.9	22	4	US-10-723-933-77 Sequence 77, Appl
55	55	80.9	22	5	US-10-471-348-13 Sequence 13, Appl
56	55	80.9	22	5	US-10-471-348-17 Sequence 17, Appl
57	55	80.9	22	5	US-10-471-348-23 Sequence 23, Appl
58	55	80.9	22	5	US-10-947-730-8 Sequence 8, Appl
59	55	80.9	22	5	US-10-947-730-9 Sequence 9, Appl
60	55	80.9	22	5	US-10-989-397-3 Sequence 3, Appl
61	55	80.9	22	6	US-11-040-810-13 Sequence 13, Appl
62	55	80.9	22	6	US-11-040-810-17 Sequence 17, Appl
63	55	80.9	22	6	US-11-040-810-23 Sequence 23, Appl
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66	55	80.9	22	6	US-11-066-697-517 Sequence 517, App
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68	55	80.9	23	6	US-11-066-697-481 Sequence 481, App
69	55	80.9	23	6	US-11-066-697-484 Sequence 484, App
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72	55	80.9	24	5	US-10-471-348-16 Sequence 16, Appl
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76	55	80.9	24	6	US-11-066-697-485 Sequence 485, App
77	55	80.9	24	6	US-11-066-697-487 Sequence 487, App
78	55	80.9	24	6	US-11-066-697-502 Sequence 502, App
79	55	80.9	24	6	US-11-066-697-505 Sequence 505, App
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83	55	80.9	25	6	US-11-066-697-480 Sequence 480, App
84	55	80.9	25	6	US-11-066-697-488 Sequence 488, App
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86	55	80.9	26	4	US-10-402-021-3 Sequence 3, Appl
87	55	80.9	26	4	US-10-723-933-35 Sequence 35, Appl
88	55	80.9	26	4	US-10-723-933-51 Sequence 51, Appl
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91	55	80.9	26	6	US-11-066-697-511 Sequence 511, App
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93	55	80.9	27	4	US-10-360-101-25 Sequence 25, Appl
94	55	80.9	27	4	US-10-360-101-88 Sequence 88, Appl
95	55	80.9	27	5	US-10-760-085-142 Sequence 142, App
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98	55	80.9	27	6	US-11-066-697-501 Sequence 501, App
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238	50	73.5	23	5	US-10-471-348-31	Sequence 31, Appli
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240	50	73.5	23	6	US-11-040-810-31	Sequence 31, Appli
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246	50	73.5	25	4	US-10-723-933-18	Sequence 18, Appli

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248	50	73.5	25	5	US-10-471-348-22	Sequence 22, Appl	321	50	73.5	36	4	US-10-723-933-80	Sequence 80, Appl
249	50	73.5	25	5	US-10-471-348-24	Sequence 24, Appl	322	50	73.5	37	4	US-10-723-933-117	Sequence 117, App
250	50	73.5	25	5	US-10-471-348-25	Sequence 25, Appl	323	50	73.5	41	3	US-09-466-268B-1	Sequence 1, Appli
251	50	73.5	25	5	US-10-471-348-26	Sequence 26, Appl	324	50	73.5	41	3	US-10-106-806-1	Sequence 1, Appli
252	50	73.5	25	6	US-11-040-810-22	Sequence 22, Appl	325	50	73.5	41	5	US-10-947-730-1	Sequence 1, Appli
253	50	73.5	25	6	US-11-040-810-24	Sequence 24, Appl	326	50	73.5	108	4	US-10-419-059-1	Sequence 1, Appli
254	50	73.5	25	6	US-11-040-810-25	Sequence 25, Appl	327	50	73.5	108	4	US-10-300-733-1	Sequence 1, Appli
255	50	73.5	25	6	US-11-040-810-26	Sequence 26, Appl	328	50	73.5	108	4	US-10-359-051-1	Sequence 1, Appli
256	50	73.5	26	3	US-09-902-517-1	Sequence 1, Appli	329	50	73.5	108	4	US-10-645-874-1	Sequence 1, Appli
257	50	73.5	26	4	US-10-106-806-7	Sequence 7, Appli	330	50	73.5	108	5	US-10-714-078-1	Sequence 1, Appli
258	50	73.5	26	4	US-10-402-021-1	Sequence 1, Appli	331	50	73.5	108	5	US-10-603-891-1	Sequence 1, Appli
259	50	73.5	26	4	US-10-723-933-107	Sequence 107, App	332	50	73.5	108	5	US-10-827-919-1	Sequence 1, Appli
260	50	73.5	26	4	US-10-723-933-124	Sequence 124, App	333	50	73.5	108	5	US-10-938-760-1	Sequence 1, Appli
261	50	73.5	26	5	US-10-471-348-27	Sequence 27, Appl	334	50	73.5	108	5	US-10-952-275-1	Sequence 1, Appli
262	50	73.5	26	5	US-10-947-730-7	Sequence 7, Appli	335	50	73.5	134	3	US-09-902-517-45	Sequence 45, Appl
263	50	73.5	26	6	US-11-040-810-27	Sequence 27, Appl	336	50	73.5	134	3	US-09-902-517-48	Sequence 48, Appl
264	50	73.5	29	4	US-10-723-933-106	Sequence 106, App	337	50	73.5	134	3	US-09-508-435-2	Sequence 2, Appli
265	50	73.5	29	4	US-10-723-933-116	Sequence 116, App	338	50	73.5	134	4	US-10-419-059-2	Sequence 2, Appli
266	50	73.5	29	4	US-10-723-933-123	Sequence 123, App	339	50	73.5	134	4	US-10-402-021-45	Sequence 45, Appl
267	50	73.5	32	3	US-09-752-724-4	Sequence 4, Appli	340	50	73.5	134	4	US-10-402-021-48	Sequence 48, Appl
268	50	73.5	32	3	US-09-466-268B-6	Sequence 6, Appli	341	50	73.5	134	4	US-10-645-874-2	Sequence 2, Appli
269	50	73.5	32	3	US-09-902-517-49	Sequence 49, Appl	342	50	73.5	134	4	US-10-714-078-2	Sequence 2, Appli
270	50	73.5	32	4	US-10-106-806-6	Sequence 6, Appli	343	50	73.5	134	5	US-10-603-891-2	Sequence 2, Appli
271	50	73.5	32	4	US-10-197-954-24	Sequence 24, Appl	344	50	73.5	134	5	US-10-723-933-22	Sequence 22, Appl
272	50	73.5	32	4	US-10-402-021-49	Sequence 49, Appl	345	50	73.5	134	5	US-10-827-919-2	Sequence 2, Appli
273	50	73.5	32	4	US-10-664-605-4	Sequence 4, Appli	346	50	73.5	134	5	US-10-952-275-2	Sequence 2, Appli
274	50	73.5	32	4	US-10-723-933-33	Sequence 33, Appl	347	50	73.5	134	5	US-10-775-204-1277	Sequence 1277, Ap
275	50	73.5	32	4	US-10-723-933-53	Sequence 53, Appl	348	50	73.5	195	4	US-10-723-933-115	Sequence 115, App
276	50	73.5	32	4	US-10-723-933-73	Sequence 73, Appl	349	50	73.5	641	5	US-10-775-204-1634	Sequence 1634, Ap
277	50	73.5	32	4	US-10-723-933-82	Sequence 82, Appl	350	50	73.5	719	5	US-10-775-204-1275	Sequence 1275, Ap
278	50	73.5	32	4	US-10-723-933-83	Sequence 83, Appl	351	49	72.1	17	4	US-10-664-605-8	Sequence 8, Appli
279	50	73.5	32	4	US-10-723-933-110	Sequence 110, App	352	49	72.1	17	4	US-10-664-605-28	Sequence 28, Appl
280	50	73.5	32	4	US-10-723-933-111	Sequence 111, App	353	49	72.1	17	4	US-10-664-605-29	Sequence 29, Appl
281	50	73.5	32	4	US-10-723-933-131	Sequence 131, App	354	49	72.1	17	4	US-10-664-605-30	Sequence 30, Appl
282	50	73.5	32	5	US-10-818-246-5	Sequence 5, Appli	355	49	72.1	17	4	US-10-664-605-36	Sequence 36, Appl
283	50	73.5	32	5	US-10-471-348-21	Sequence 21, Appl	356	49	72.1	17	4	US-10-664-605-70	Sequence 70, Appl
284	50	73.5	32	5	US-10-471-348-45	Sequence 45, Appl	357	49	72.1	32	5	US-10-471-348-57	Sequence 57, Appl
285	50	73.5	32	5	US-10-471-348-46	Sequence 46, Appl	358	49	72.1	32	6	US-11-040-810-57	Sequence 57, Appl
286	50	73.5	32	5	US-10-471-348-48	Sequence 48, Appl	359	48	70.6	17	3	US-09-902-517-5	Sequence 5, Appli
287	50	73.5	32	5	US-10-471-348-49	Sequence 49, Appl	360	48	70.6	17	4	US-10-402-021-5	Sequence 5, Appli
288	50	73.5	32	5	US-10-471-348-51	Sequence 51, Appl	361	48	70.6	17	4	US-10-664-605-25	Sequence 25, Appl
289	50	73.5	32	5	US-10-471-348-52	Sequence 52, Appl	362	48	70.6	17	4	US-10-664-605-26	Sequence 26, Appl
290	50	73.5	32	5	US-10-471-348-54	Sequence 54, Appl	363	48	70.6	17	4	US-10-664-605-32	Sequence 32, Appl
291	50	73.5	32	5	US-10-471-348-56	Sequence 56, Appl	364	48	70.6	17	4	US-10-664-605-33	Sequence 33, Appl
292	50	73.5	32	5	US-10-760-085-24	Sequence 24, Appl	365	48	70.6	17	4	US-10-664-605-71	Sequence 71, Appl
293	50	73.5	32	5	US-10-947-730-6	Sequence 6, Appli	366	48	70.6	23	4	US-10-106-806-11	Sequence 11, Appl
294	50	73.5	32	5	US-10-989-397-2	Sequence 2, Appli	367	48	70.6	23	5	US-10-947-730-11	Sequence 11, Appl
295	50	73.5	32	5	US-10-775-204-1802	Sequence 1802, Ap	368	48	70.6	28	5	US-10-471-348-11	Sequence 11, Appl
296	50	73.5	32	6	US-11-040-810-21	Sequence 21, Appl	369	48	70.6	28	5	US-10-471-348-19	Sequence 19, Appl
297	50	73.5	32	6	US-11-040-810-45	Sequence 45, Appl	370	48	70.6	28	5	US-10-471-348-20	Sequence 20, Appl
298	50	73.5	32	6	US-11-040-810-46	Sequence 46, Appl	371	48	70.6	28	6	US-11-040-810-11	Sequence 11, Appl
299	50	73.5	32	6	US-11-040-810-48	Sequence 48, Appl	372	48	70.6	28	6	US-11-040-810-19	Sequence 19, Appl
300	50	73.5	32	6	US-11-040-810-49	Sequence 49, Appl	373	48	70.6	28	6	US-11-040-810-20	Sequence 20, Appl
301	50	73.5	32	6	US-11-040-810-51	Sequence 51, Appl	374	48	70.6	33	6	US-11-066-697-515	Sequence 515, App
302	50	73.5	32	6	US-11-040-810-52	Sequence 52, Appl	375	48	70.6	38	3	US-09-466-268B-10	Sequence 10, Appl
303	50	73.5	32	6	US-11-040-810-54	Sequence 54, Appl	376	48	70.6	38	4	US-10-106-806-10	Sequence 10, Appl
304	50	73.5	32	6	US-11-040-810-56	Sequence 56, Appl	377	48	70.6	38	4	US-10-723-933-76	Sequence 76, Appl
305	50	73.5	32	6	US-11-066-697-509	Sequence 509, App	378	48	70.6	38	5	US-10-947-730-10	Sequence 10, Appl
306	50	73.5	32	6	US-11-066-697-516	Sequence 516, App	379	47	69.1	17	4	US-10-664-605-6	Sequence 6, Appli
307	50	73.5	33	3	US-09-942-709-1	Sequence 1, Appli	380	47	69.1	17	4	US-10-664-605-7	Sequence 7, Appli
308	50	73.5	33	4	US-10-723-933-5	Sequence 5, Appli	381	47	69.1	17	4	US-10-664-605-34	Sequence 34, Appl
309	50	73.5	33	4	US-10-723-933-108	Sequence 108, App	382	46	67.6	17	4	US-10-664-605-38	Sequence 38, Appl
310	50	73.5	33	4	US-10-723-933-112	Sequence 112, App	383	46	67.6	17	4	US-10-664-605-39	Sequence 39, Appl
311	50	73.5	33	5	US-10-697-886-1	Sequence 1, Appli	384	46	67.6	21	3	US-09-466-268B-8	Sequence 8, Appli
312	50	73.5	33	5	US-10-471-348-47	Sequence 47, Appl	385	46	67.6	22	5	US-10-471-348-14	Sequence 14, Appl
313	50	73.5	33	5	US-10-471-348-50	Sequence 50, Appl	386	46	67.6	22	5	US-10-471-348-18	Sequence 18, Appl
314	50	73.5	33	5	US-10-471-348-53	Sequence 53, Appl	387	46	67.6	22	6	US-11-040-810-14	Sequence 14, Appl
315	50	73.5	33	5	US-10-471-348-55	Sequence 55, Appl	388	46	67.6	22	6	US-11-040-810-18	Sequence 18, Appl
316	50	73.5	33	6	US-11-040-810-47	Sequence 47, Appl	389	46	67.6	85	4	US-10-425-115-348455	Sequence 348455,
317	50	73.5	33	6	US-11-040-810-50	Sequence 50, Appl	390	43	63.2	17	4	US-10-723-933-2	Sequence 2, Appli
318	50	73.5	33	6	US-11-040-810-53	Sequence 53, Appl	391	43	63.2	17	4	US-10-723-933-109	Sequence 109, App
319	50	73.5	33	6	US-11-040-810-55	Sequence 55, Appl	392	43	63.2	23	5	US-10-471-348-34	Sequence 34, Appl

393	43	63.2	23	5	US-10-471-348-35	Sequence 35, Appl	466	33	48.5	562	4	US-10-437-963-157091	Sequence 157091,
394	43	63.2	23	6	US-11-040-810-34	Sequence 34, Appl	467	33	48.5	781	4	US-10-437-963-176775	Sequence 176775,
395	43	63.2	23	6	US-11-040-810-35	Sequence 35, Appl	468	32	47.1	17	5	US-10-471-348-40	Sequence 40, Appl
396	43	63.2	24	5	US-10-471-348-36	Sequence 36, Appl	469	32	47.1	17	5	US-10-471-348-43	Sequence 43, Appl
397	43	63.2	24	6	US-11-040-810-36	Sequence 36, Appl	470	32	47.1	17	6	US-11-040-810-40	Sequence 40, Appl
398	43	63.2	26	4	US-10-723-933-113	Sequence 113, App	471	32	47.1	17	6	US-11-040-810-43	Sequence 43, Appl
399	43	63.2	32	5	US-10-471-348-37	Sequence 37, Appl	472	32	47.1	87	3	US-09-764-891-2746	Sequence 2746, Ap
400	43	63.2	32	6	US-11-040-810-37	Sequence 37, Appl	473	32	47.1	91	4	US-10-630-590-203	Sequence 203, App
401	43	63.2	33	5	US-10-471-348-38	Sequence 38, Appl	474	32	47.1	91	5	US-10-789-102-302	Sequence 302, App
402	43	63.2	33	6	US-11-040-810-38	Sequence 38, Appl	475	32	47.1	91	6	US-11-021-949-332	Sequence 332, App
403	43	63.2	37	4	US-10-723-933-136	Sequence 136, App	476	32	47.1	91	6	US-11-021-928A-229	Sequence 229, App
404	42	61.8	14	4	US-10-664-605-14	Sequence 14, Appl	477	32	47.1	93	5	US-10-938-249-284	Sequence 284, App
405	42	61.8	14	4	US-10-664-605-15	Sequence 15, Appl	478	32	47.1	175	4	US-10-767-701-51260	Sequence 51260, A
406	41	60.3	17	5	US-10-471-348-39	Sequence 39, Appl	479	32	47.1	178	4	US-10-425-115-220696	Sequence 220696,
407	41	60.3	17	5	US-10-471-348-42	Sequence 42, Appl	480	32	47.1	223	4	US-10-425-115-272422	Sequence 272422,
408	41	60.3	17	6	US-11-040-810-39	Sequence 39, Appl	481	32	47.1	317	4	US-10-282-122A-49359	Sequence 49359, A
409	41	60.3	17	6	US-11-040-810-42	Sequence 42, Appl	482	32	47.1	321	4	US-10-306-762-209	Sequence 209, App
410	41	60.3	23	5	US-10-471-348-39	Sequence 29, Appl	483	32	47.1	323	4	US-10-306-762-216	Sequence 216, App
411	41	60.3	23	5	US-10-471-348-32	Sequence 32, Appl	484	32	47.1	355	5	US-10-739-930-9926	Sequence 9926, Ap
412	41	60.3	23	6	US-11-040-810-29	Sequence 29, Appl	485	32	47.1	442	5	US-10-732-923-23732	Sequence 23732, A
413	41	60.3	23	6	US-11-040-810-32	Sequence 32, Appl	486	32	47.1	443	5	US-10-732-923-23762	Sequence 23762, A
414	41	60.3	25	3	US-09-466-268B-7	Sequence 7, Appli	487	32	47.1	444	5	US-10-732-923-11220	Sequence 11220, A
415	41	60.3	28	4	US-10-723-933-135	Sequence 135, App	488	32	47.1	446	5	US-10-732-923-23745	Sequence 23745, A
416	41	60.3	32	4	US-10-360-101-86	Sequence 86, Appl	489	32	47.1	459	4	US-10-369-493-18259	Sequence 18259, A
417	40.5	59.6	42	4	US-10-279-061-74	Sequence 74, Appl	490	32	47.1	459	5	US-10-732-923-11215	Sequence 11215, A
418	40	58.8	17	4	US-10-664-605-27	Sequence 27, Appl	491	32	47.1	463	4	US-10-311-765-2	Sequence 2, Appli
419	40	58.8	21	6	US-11-066-697-496	Sequence 496, App	492	32	47.1	488	5	US-10-408-765A-1522	Sequence 1522, Ap
420	39	57.4	11	4	US-10-664-605-22	Sequence 22, Appl	493	32	47.1	488	5	US-10-732-923-23757	Sequence 23757, A
421	39	57.4	12	4	US-10-664-605-21	Sequence 21, Appl	494	32	47.1	514	3	US-09-987-701-12	Sequence 12, Appl
422	39	57.4	13	4	US-10-664-605-16	Sequence 16, Appl	495	32	47.1	514	3	US-09-987-701-12	Sequence 12, Appl
423	39	57.4	13	4	US-10-664-605-17	Sequence 17, Appl	496	32	47.1	514	5	US-10-631-467-765	Sequence 765, App
424	39	57.4	13	4	US-10-664-605-18	Sequence 18, Appl	497	32	47.1	514	5	US-10-631-467-1515	Sequence 1515, Ap
425	39	57.4	13	4	US-10-664-605-19	Sequence 19, Appl	498	32	47.1	524	4	US-10-437-963-159034	Sequence 159034,
426	39	57.4	15	6	US-11-066-697-493	Sequence 493, App	499	32	47.1	544	5	US-10-732-923-11300	Sequence 11300, A
427	39	57.4	17	4	US-10-664-605-24	Sequence 24, Appl	500	32	47.1	547	4	US-10-437-963-192947	Sequence 192947,
428	39	57.4	22	3	US-09-466-268B-11	Sequence 11, Appl	501	32	47.1	552	4	US-10-282-122A-49450	Sequence 49450, A
429	38	55.9	28	4	US-10-723-933-41	Sequence 41, Appl	502	32	47.1	552	4	US-10-282-122A-50601	Sequence 50601, A
430	37	54.4	18	3	US-09-027-777B-9	Sequence 9, Appli	503	32	47.1	558	4	US-10-282-122A-51345	Sequence 51345, A
431	37	54.4	21	6	US-11-066-697-494	Sequence 494, App	504	32	47.1	559	4	US-10-343-251A-7	Sequence 7, Appli
432	35	51.5	48	4	US-10-424-599-238575	Sequence 238575,	505	32	47.1	559	5	US-10-239-032-3	Sequence 3, Appli
433	35	51.5	540	4	US-10-156-761-9568	Sequence 9568, Ap	506	32	47.1	576	4	US-10-275-505-5	Sequence 5, Appli
434	35	51.5	1289	4	US-10-424-599-204412	Sequence 204412,	507	32	47.1	576	6	US-11-140-224-5	Sequence 5, Appli
435	35	51.5	2110	5	US-10-732-923-20533	Sequence 20533, A	508	32	47.1	731	4	US-10-275-107-52	Sequence 52, Appl
436	35	51.5	2116	5	US-10-732-923-20537	Sequence 20537, A	509	32	47.1	737	3	US-09-877-843-10	Sequence 10, Appl
437	35	51.5	2118	5	US-10-732-923-20538	Sequence 20538, A	510	31	45.6	34	3	US-09-864-761-47305	Sequence 47305, A
438	34	50.0	62	4	US-10-424-599-261170	Sequence 261170,	511	31	45.6	70	3	US-09-864-408A-4220	Sequence 4220, Ap
439	34	50.0	129	4	US-10-469-821-2	Sequence 2, Appli	512	31	45.6	75	4	US-10-327-514-14	Sequence 14, Appl
440	34	50.0	194	4	US-10-437-963-145208	Sequence 145208,	513	31	45.6	75	5	US-10-499-762-14	Sequence 14, Appl
441	34	50.0	235	4	US-10-437-963-104005	Sequence 104005,	514	31	45.6	78	4	US-10-425-115-217135	Sequence 217135,
442	34	50.0	494	5	US-10-732-923-11146	Sequence 11146, A	515	31	45.6	79	4	US-10-425-115-232838	Sequence 232838,
443	34	50.0	526	4	US-10-437-963-198767	Sequence 198767,	516	31	45.6	84	4	US-10-424-599-146758	Sequence 146758,
444	34	50.0	526	5	US-10-481-113-20	Sequence 20, Appl	517	31	45.6	85	4	US-10-437-963-102947	Sequence 102947,
445	34	50.0	526	5	US-10-732-923-11241	Sequence 11241, A	518	31	45.6	144	4	US-10-425-114-69116	Sequence 69116, A
446	34	50.0	526	5	US-10-481-032A-48	Sequence 48, Appl	519	31	45.6	144	4	US-10-425-115-303576	Sequence 303576,
447	34	50.0	531	5	US-10-732-923-11287	Sequence 11287, A	520	31	45.6	149	4	US-10-424-599-199305	Sequence 199305,
448	34	50.0	545	5	US-10-732-923-11256	Sequence 11256, A	521	31	45.6	166	5	US-10-795-159-707	Sequence 707, App
449	34	50.0	648	4	US-10-408-765A-2690	Sequence 2690, Ap	522	31	45.6	175	4	US-10-425-115-339534	Sequence 339534,
450	33.5	49.3	270	4	US-10-437-963-116692	Sequence 116692,	523	31	45.6	193	4	US-10-437-963-118966	Sequence 118966,
451	33.5	49.3	486	6	US-11-097-143-5976	Sequence 5976, Ap	524	31	45.6	193	5	US-10-287-436A-219	Sequence 219, App
452	33	48.5	15	4	US-10-664-605-11	Sequence 11, Appl	525	31	45.6	197	4	US-10-424-599-207929	Sequence 207929,
453	33	48.5	15	4	US-10-664-605-13	Sequence 13, Appl	526	31	45.6	260	4	US-10-282-122A-66290	Sequence 66290, A
454	33	48.5	97	4	US-10-425-114-44256	Sequence 44256, A	527	31	45.6	269	4	US-10-282-122A-47304	Sequence 47304, A
455	33	48.5	117	4	US-10-425-115-318910	Sequence 318910,	528	31	45.6	286	4	US-10-424-599-234129	Sequence 234129,
456	33	48.5	229	4	US-10-424-599-181155	Sequence 181155,	529	31	45.6	316	4	US-10-437-963-126807	Sequence 126807,
457	33	48.5	252	4	US-10-369-493-7843	Sequence 7843, Ap	530	31	45.6	360	4	US-10-437-963-126811	Sequence 126811,
458	33	48.5	343	4	US-10-425-115-336600	Sequence 336600,	531	31	45.6	393	4	US-10-369-493-18918	Sequence 18918, A
459	33	48.5	424	5	US-10-732-923-11257	Sequence 11257, A	532	31	45.6	400	5	US-10-732-923-11195	Sequence 11195, A
460	33	48.5	429	4	US-10-425-115-188229	Sequence 188229	533	31	45.6	405	4	US-10-282-122A-67109	Sequence 67109, A
461	33	48.5	447	4	US-10-425-114-37618	Sequence 37618, A	534	31	45.6	407	3	US-09-815-242-11180	Sequence 11180, A
462	33	48.5	519	4	US-10-425-115-306500	Sequence 306500,	535	31	45.6	407	3	US-10-282-122A-58406	Sequence 58406, A
463	33	48.5	526	4	US-10-425-115-326033	Sequence 326033,	536	31	45.6	407	4	US-10-282-122A-58406	Sequence 58406, A
464	33	48.5	539	5	US-10-732-923-11152	Sequence 11152, A	537	31	45.6	419	6	US-11-097-143-37002	Sequence 37002, A
465	33	48.5	541	4	US-10-425-114-50689	Sequence 50689, A	538	31	45.6	422	4	US-10-369-493-8491	Sequence 8491, Ap

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540	31	45.6	440	4	US-10-374-780A-1132	Sequence 1132, Ap	613	30	44.1	280	5	US-10-739-930-6124	Sequence 6124, Ap
541	31	45.6	441	4	US-10-412-699B-1331	Sequence 1331, Ap	614	30	44.1	285	4	US-10-017-161-1770	Sequence 1770, Ap
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548	31	45.6	480	5	US-10-469-204-152	Sequence 152, App	621	30	44.1	374	4	US-10-437-963-132693	Sequence 132693, A
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597	30	44.1	140	4	US-10-425-115-328995	Sequence 328995, A	670	30	44.1	521	5	US-10-732-923-11155	Sequence 11155, A
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727	30	44.1	823	4	US-10-142-885-379	Sequence 379, App
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737	30	44.1	833	4	US-10-226-318-5	Sequence 5, Appl1
738	30	44.1	833	4	US-10-648-786-5	Sequence 5, Appl1
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754	30	44.1	1893	4	US-10-137-871-89	Sequence 89, Appl
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783	30	44.1	2033	4	US-10-140-864-307	Sequence 307, App
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788	30	44.1	2542	4	US-10-146-731-95	Sequence 95, Appl
789	30	44.1	2542	4	US-10-140-472-95	Sequence 95, Appl
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793	30	44.1	2542	4	US-10-137-871-95	Sequence 95, Appl
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812	30	44.1	2956	4	US-10-141-756-15	Sequence 15, Appl
813	30	44.1	2956	4	US-10-141-759-15	Sequence 15, Appl
814	30	44.1	2956	4	US-10-140-805-15	Sequence 15, Appl
815	30	44.1	3127	4	US-10-184-644-83	Sequence 83, Appl
816	30	44.1	3127	4	US-10-184-634-83	Sequence 83, Appl
817	30	44.1	35823	5	US-10-874-049-1	Sequence 1, Appl1
818	29.5	43.4	127	4	US-10-424-599-179777	Sequence 179777, A
819	29.5	43.4	166	4	US-10-424-599-237589	Sequence 237589, A
820	29	42.6	9	4	US-10-327-514-16	Sequence 16, Appl
821	29	42.6	9	5	US-10-499-762-16	Sequence 16, Appl
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825	29	42.6	26	5	US-10-499-762-25	Sequence 25, Appl
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827	29	42.6	51	4	US-10-327-514-21	Sequence 21, Appl
828	29	42.6	51	5	US-10-499-762-21	Sequence 21, Appl
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830	29	42.6	70	4	US-10-425-115-197489	Sequence 197489, A

831	29	42.6	71	4	US-10-269-806-42	Sequence 42, Appl	904	29	42.6	438	4	US-10-282-122A-43302	Sequence 43302, A
832	29	42.6	73	4	US-10-437-963-130652	Sequence 130652,	905	29	42.6	438	4	US-10-282-122A-55742	Sequence 55742, A
833	29	42.6	79	4	US-10-437-963-183363	Sequence 183363,	906	29	42.6	449	5	US-10-732-923-11216	Sequence 11216, A
834	29	42.6	81	4	US-10-424-599-215166	Sequence 215166,	907	29	42.6	455	4	US-10-282-122A-60545	Sequence 60545, A
835	29	42.6	104	4	US-10-425-115-256733	Sequence 256733,	908	29	42.6	456	4	US-10-038-854-164	Sequence 164, App
836	29	42.6	106	4	US-10-327-514-20	Sequence 20, Appl	909	29	42.6	462	3	US-09-738-626-5120	Sequence 5120, App
837	29	42.6	106	5	US-10-499-762-20	Sequence 20, Appl	910	29	42.6	462	4	US-10-627-476-502	Sequence 502, App
838	29	42.6	108	4	US-10-425-115-234271	Sequence 234271,	911	29	42.6	465	5	US-10-732-923-11316	Sequence 11316, A
839	29	42.6	111	4	US-10-437-963-133254	Sequence 133254,	912	29	42.6	466	4	US-10-238-075-480	Sequence 480, App
840	29	42.6	124	4	US-10-437-963-133254	Sequence 133254,	913	29	42.6	467	5	US-10-501-282-5212	Sequence 5212, App
841	29	42.6	129	4	US-10-131-410-129	Sequence 129, App	914	29	42.6	481	4	US-10-437-963-183222	Sequence 183222,
842	29	42.6	130	4	US-10-327-514-10	Sequence 10, Appl	915	29	42.6	483	4	US-10-437-963-122266	Sequence 122266,
843	29	42.6	130	5	US-10-499-762-10	Sequence 10, Appl	916	29	42.6	484	4	US-10-425-115-196844	Sequence 196844,
844	29	42.6	132	4	US-10-327-514-11	Sequence 11, Appl	917	29	42.6	486	5	US-10-450-763-46209	Sequence 46209, A
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846	29	42.6	132	4	US-10-327-514-15	Sequence 15, Appl	919	29	42.6	490	4	US-10-156-761-13366	Sequence 13366, A
847	29	42.6	132	4	US-10-767-701-43246	Sequence 43246, A	920	29	42.6	493	4	US-10-282-122A-44867	Sequence 44867, A
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850	29	42.6	132	5	US-10-499-762-15	Sequence 15, Appl	923	29	42.6	514	5	US-10-732-923-23856	Sequence 23856, A
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852	29	42.6	133	4	US-10-327-514-13	Sequence 13, Appl	925	29	42.6	532	4	US-10-369-493-19435	Sequence 19435, A
853	29	42.6	133	5	US-10-499-762-9	Sequence 9, Appl	926	29	42.6	534	4	US-10-038-854-28	Sequence 28, Appl
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862	29	42.6	189	4	US-10-264-237-2466	Sequence 2466, Ap	935	29	42.6	556	5	US-10-968-848-80	Sequence 80, Appl
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873	29	42.6	264	5	US-10-450-763-57098	Sequence 57098, A	946	29	42.6	695	4	US-10-184-644-567	Sequence 567, App
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876	29	42.6	312	5	US-10-450-763-41248	Sequence 41248, A	949	29	42.6	696	4	US-10-437-963-152744	Sequence 152744,
877	29	42.6	316	4	US-10-425-114-57324	Sequence 57324, A	950	29	42.6	696	5	US-10-415-187-7	Sequence 7, Appli
878	29	42.6	319	4	US-10-306-762-204	Sequence 204, App	951	29	42.6	788	4	US-10-239-391B-2	Sequence 2, Appli
879	29	42.6	324	4	US-10-437-963-122666	Sequence 122666,	952	29	42.6	792	4	US-10-282-122A-47546	Sequence 47546, A
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881	29	42.6	338	4	US-10-425-114-68695	Sequence 68695, A	954	29	42.6	816	4	US-10-450-763-42829	Sequence 42829, A
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883	29	42.6	361	4	US-10-094-749-3049	Sequence 3049, Ap	956	29	42.6	869	4	US-10-437-963-189803	Sequence 189803,
884	29	42.6	361	4	US-10-038-854-165	Sequence 165, App	957	29	42.6	972	4	US-10-369-493-11947	Sequence 11947, A
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886	29	42.6	373	4	US-10-282-122A-47451	Sequence 47451, A	959	29	42.6	999	4	US-10-123-155-395	Sequence 395, App
887	29	42.6	378	4	US-10-369-493-5080	Sequence 5080, Ap	960	29	42.6	999	4	US-10-146-731-395	Sequence 395, App
888	29	42.6	386	5	US-10-732-923-11268	Sequence 11268, A	961	29	42.6	999	4	US-10-140-472-395	Sequence 395, App
889	29	42.6	393	5	US-10-739-930-7212	Sequence 7212, Ap	962	29	42.6	999	4	US-10-141-761-395	Sequence 395, App
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892	29	42.6	400	5	US-10-450-763-55885	Sequence 55885, A	965	29	42.6	999	4	US-10-137-871-395	Sequence 395, App
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894	29	42.6	419	3	US-09-741-669-415	Sequence 415, App	967	29	42.6	999	4	US-10-141-756-395	Sequence 395, App
895	29	42.6	419	4	US-10-369-493-23477	Sequence 23477, A	968	29	42.6	999	4	US-10-141-759-395	Sequence 395, App
896	29	42.6	419	4	US-10-038-854-371	Sequence 371, App	969	29	42.6	999	4	US-10-140-805-395	Sequence 395, App
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898	29	42.6	431	3	US-10-494-541-50	Sequence 50, Appl	971	29	42.6	1015	6	US-11-097-143-24927	Sequence 24927, A
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901	29	42.6	431	4	US-10-425-114-51428	Sequence 51428, A	974	29	42.6	1355	4	US-10-146-731-421	Sequence 421, App
902	29	42.6	434	4	US-10-282-122A-60268	Sequence 60268, A	975	29	42.6	1355	4	US-10-140-472-421	Sequence 421, App
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979	29	42.6	1355	4	US-10-137-871-421	Sequence 421, App
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981	29	42.6	1355	4	US-10-141-756-421	Sequence 421, App
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984	29	42.6	1355	4	US-10-140-864-421	Sequence 421, App
985	29	42.6	1356	4	US-10-123-155-43	Sequence 43, Appl
986	29	42.6	1356	4	US-10-146-731-43	Sequence 43, Appl
987	29	42.6	1356	4	US-10-140-472-43	Sequence 43, Appl
988	29	42.6	1356	4	US-10-141-761-43	Sequence 43, Appl
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990	29	42.6	1356	4	US-10-158-790-43	Sequence 43, Appl
991	29	42.6	1356	4	US-10-137-871-43	Sequence 43, Appl
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993	29	42.6	1356	4	US-10-141-756-43	Sequence 43, Appl
994	29	42.6	1356	4	US-10-141-759-43	Sequence 43, Appl
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997	29	42.6	1356	4	US-10-437-963-107743	Sequence 107743,
998	29	42.6	1410	4	US-10-184-644-123	Sequence 123, App
999	29	42.6	1410	4	US-10-184-634-123	Sequence 123, App
1000	29	42.6	1422	4	US-10-123-155-117	Sequence 117, App

ALIGNMENTS

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RESULT 1
US-10-664-605-10
; Sequence 10, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-10
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Query Match      82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Db      1 CFGKLDRIGSASGLGC 17

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US-10-664-605-40
; Sequence 40, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
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; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-40

Query Match      82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Db      1 CFGAKLDRIGSMSGLGC 17
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RESULT 3
US-10-664-605-45
; Sequence 45, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-45
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Query Match      82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Db      1 CFGKADRI GSM SGLGC 17

RESULT 4
US-10-664-605-58
; Sequence 58, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
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APPLICANT: Golembio, Myriam
APPLICANT: Yayon, Avner
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
FILE REFERENCE: PRO/011/US
CURRENT APPLICATION NUMBER: US/10/664,605
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: US 60/276,939
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: IL 142118
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: PCT/IL02/00229
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide variant
US-10-664-605-58

Query Match 82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 1 CFGKLDRIGSMSALGC 17

RESULT 5

US-10-664-605-63
Sequence 63, Application US/10664605
Publication No. US20040138134A1
GENERAL INFORMATION:
APPLICANT: Prochon Biotech Ltd.
APPLICANT: Golembio, Myriam
APPLICANT: Yayon, Avner
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
FILE REFERENCE: PRO/011/US
CURRENT APPLICATION NUMBER: US/10/664,605
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: US 60/276,939
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: IL 142118
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: PCT/IL02/00229
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide variant
US-10-664-605-63

Query Match 82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
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Db 1 CFGKLDRIGSMSGAGC 17

RESULT 6
US-10-664-605-68
Sequence 68, Application US/10664605
Publication No. US20040138134A1
GENERAL INFORMATION:

APPLICANT: Prochon Biotech Ltd.
APPLICANT: Golembio, Myriam
APPLICANT: Yayon, Avner
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
FILE REFERENCE: PRO/011/US
CURRENT APPLICATION NUMBER: US/10/664,605
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: US 60/276,939
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: IL 142118
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: PCT/IL02/00229
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide variant
US-10-664-605-68

Query Match 82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 1 CFGKLDRIGSSSGLGC 17

RESULT 7

US-11-066-697-469
Sequence 469, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 469
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-469

Query Match 82.4%; Score 56; DB 6; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 1 CFGSRIDRIGAQSGMGC 17

RESULT 8

US-11-066-697-470
; Sequence 470, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 470
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-470

Query Match 82.4%; Score 56; DB 6; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17

Db 1 CFGSRIDRIGAQSGMGC 17

RESULT 9

US-09-752-724-5
; Sequence 5, Application US/09752724
; Patent No. US20010027181A1
; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; TITLE OF INVENTION: ISCHEMIC HEART DISEASE
; FILE REFERENCE: PP/S-38-252US
; CURRENT APPLICATION NUMBER: US/09/752,724
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: frog
US-09-752-724-5

Query Match 82.4%; Score 56; DB 3; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17

Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 10

US-11-066-697-468
; Sequence 468, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 468
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-468

Query Match 82.4%; Score 56; DB 6; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17

Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 11

US-11-066-697-471
; Sequence 471, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 471
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide

US-11-066-697-471

Query Match 82.4%; Score 56; DB 6; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 4 CFGSRIDRIGAGSGMGC 20

RESULT 12

US-11-066-697-472

; Sequence 472, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:

; APPLICANT: Bridon, Dominique P.

; APPLICANT: Ezrin, Alan M.

; APPLICANT: Milner, Peter G.

; APPLICANT: Holmes, Darren L.

; APPLICANT: Thibaudau, Karen

; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM

; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD

; TITLE OF INVENTION: COMPONENTS

; FILE REFERENCE: 500862002301

; CURRENT APPLICATION NUMBER: US/11/066,697

; PRIOR FILING DATE: 2005-02-25

; PRIOR APPLICATION NUMBER: 09/657,276

; PRIOR FILING DATE: 2000-09-07

; PRIOR APPLICATION NUMBER: 60/153,406

; PRIOR FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: 60/159,783

; PRIOR FILING DATE: 1999-10-15

; NUMBER OF SEQ ID NOS: 1617

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 472

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-11-066-697-472

Query Match 82.4%; Score 56; DB 6; Length 30;
Best Local Similarity 58.8%; Pred. No. 0.00052;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 11 CFGSRIDRIGAGSGMGC 27

RESULT 13

US-09-902-517-15

; Sequence 15, Application US/09902517
; Publication No. US20030109430A1
; GENERAL INFORMATION:

; APPLICANT: Seilhamer, Jeffrey J.

; APPLICANT: Lewicki, John

; APPLICANT: Scarborough, Robert M.

; APPLICANT: Porter, Gordon J.

; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN

; TITLE OF INVENTION: NATRIURETIC PEPTIDE

; FILE REFERENCE: 219002025213

; CURRENT APPLICATION NUMBER: US/09/902,517

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: 09/287,892

; PRIOR FILING DATE: 1999-04-07

; PRIOR APPLICATION NUMBER: 08/850,910

; PRIOR FILING DATE: 1997-05-05

; PRIOR APPLICATION NUMBER: 07/477,226

; PRIOR FILING DATE: 1990-02-08

; PRIOR APPLICATION NUMBER: 07/299,880

; PRIOR FILING DATE: 1989-01-19

; PRIOR APPLICATION NUMBER: 07/206,470

; PRIOR FILING DATE: 1988-06-14

; PRIOR APPLICATION NUMBER: 07/200,383

; PRIOR FILING DATE: 1988-05-31

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Proviso formula (1)

US-09-902-517-15

Query Match 80.9%; Score 55; DB 3; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 1 CFGRRIDRIGSLGLGC 17

RESULT 14

US-09-027-777B-1

; Sequence 1, Application US/0902777B

; Publication No. US20030171536A1

; GENERAL INFORMATION:

; APPLICANT: IMMER, Hansueli

; APPLICANT: FORSMANN, Wolf-Georg

; APPLICANT: ADERMAN, Knut

; APPLICANT: KLESSEN, Christian

; TITLE OF INVENTION: PROCESS AND INTERMEDIATE PRODUCTS FOR

; TITLE OF INVENTION: PREPARING CARDIODILATIN FRAGMENTS AND HIGHLY PURIFIED CARDIOPE

; TITLE OF INVENTION: FRAGMENTS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

; STREET: 655 Fifteenth Street, N.W., Suite 330

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-4810

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/027,777B

; FILING DATE: 23-FEB-1998

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 44 20 381.0

; FILING DATE: 02-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 195 13 784.1

; FILING DATE: 10-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitz, Monica C.

; REGISTRATION NUMBER: 36,105

; REFERENCE/DOCKET NUMBER: P1614-8019

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-5000

; TELEFAX: (202) 368-4810

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-09-027-777B-1

Query Match 80.9%; Score 55; DB 3; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 1 CFGGRMDRIGAGSGLGC 17

RESULT 15

US-10-327-514-17
; Sequence 17, Application US/10327514
; Publication No. US20030125258A1
; GENERAL INFORMATION:
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFFATT, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 544172000100
; CURRENT APPLICATION NUMBER: US/10/327,514
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-327-514-17

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 1 CFGGRIDRIGAGSGLGC 17

RESULT 16

US-10-327-514-18
; Sequence 18, Application US/10327514
; Publication No. US20030125258A1
; GENERAL INFORMATION:
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFFATT, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 544172000100
; CURRENT APPLICATION NUMBER: US/10/327,514
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-327-514-18

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 1 CFGGRIDRIGAGSGLGC 17

RESULT 17

US-10-327-514-19
; Sequence 19, Application US/10327514
; Publication No. US20030125258A1
; GENERAL INFORMATION:
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFFATT, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 544172000100
; CURRENT APPLICATION NUMBER: US/10/327,514
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-327-514-19

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 1 CFGKLDRIGSMGLGC 17

RESULT 18

US-10-402-021-15
; Sequence 15, Application US/10402021
; Publication No. US20040002458A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING NATRIURETIC PEPTIDE
; TITLE OF INVENTION: (AMENDED)
; FILE REFERENCE: 219002025203
; CURRENT APPLICATION NUMBER: US/10/402,021
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Proviso formula (1)
US-10-402-021-15

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17

Db 1 CFGRRLDRIGSLGCG 17

RESULT 19

US-10-664-605-2
; Sequence 2, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: P23582
; DATABASE ENTRY DATE: 2001-10-16
; RELEVANT RESIDUES: (110)..(126)
US-10-664-605-2

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 1 CFGKLDRIGSMGLGC 17

RESULT 20

US-10-664-605-41
; Sequence 41, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-41

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CFGXXXDRIGXXSXGC 17
Db 1 CFGIKLDRIGSMGLGC 17

RESULT 21

US-10-664-605-42
; Sequence 42, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-42

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 1 CFGVKLDRIGSMGLGC 17

RESULT 22

US-10-664-605-43
; Sequence 43, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-43

Query Match 80.9%; Score 55; DB 4; Length 17;

Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXSXXGC 17
||| ||| | ||
Db 1 CFGLLDRIGMSGGLGC 17

RESULT 23

US-10-664-605-44
; Sequence 44, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-44

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXSXXGC 17
||| ||| | ||
Db 1 CFGMLDRIGMSGGLGC 17

RESULT 24

US-10-664-605-46
; Sequence 46, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-46

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXSXXGC 17
||| ||| | ||
Db 1 CFGLKIDRIGMSGGLGC 17

RESULT 25

US-10-664-605-47
; Sequence 47, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-47

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXSXXGC 17
||| ||| | ||
Db 1 CFGUKVDRIGMSGGLGC 17

RESULT 26

US-10-664-605-54
; Sequence 54, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-54

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 1 CFGKLDRIGMSGIGC 17

RESULT 27

US-10-664-605-56
; Sequence 56, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-56

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 1 CFGKLDRIGMSGIGC 17

RESULT 28

US-10-664-605-59
; Sequence 59, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant

US-10-664-605-59

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 1 CFGKLDRIGMSGIGC 17

RESULT 29

US-10-664-605-60
; Sequence 60, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-60

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 1 CFGKLDRIGMSGIGC 17

RESULT 30

US-10-664-605-61
; Sequence 61, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: peptide variant
US-10-664-605-61

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXSXXGC 17
||| ||||| | ||
Db 1 CFGKLDRIGMSGGC 17

RESULT 31

US-10-664-605-62
; Sequence 62, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-62

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXSXXGC 17
||| ||||| | ||
Db 1 CFGKLDRIGMSGGC 17

RESULT 32

US-10-664-605-64
; Sequence 64, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-64

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXSXXGC 17
||| ||||| | ||
Db 1 CFGKLDRIGMSGGC 17

RESULT 33

US-10-664-605-66
; Sequence 66, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-66

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXSXXGC 17
||| ||||| | ||
Db 1 CFGKLDRIGSHSLGC 17

RESULT 34

US-10-664-605-67
; Sequence 67, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 17
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-67

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| ||| |||
Db 1 CFGKLDRIGSKSGLGC 17

RESULT 35
US-10-664-605-69

; Sequence 69, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-69

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| ||| |||
Db 1 CFGKLDRIGSGSLGC 17

RESULT 36

US-10-499-762-17
; Sequence 17, Application US/10499762
; Publication No. US20050143562A1
; GENERAL INFORMATION:
; APPLICANT: PHENOGENE THERAPEUTICS INC.
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFATY, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 09680.0252USWO
; CURRENT APPLICATION NUMBER: US/10/499,762
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/IB02/05778
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 17
; LENGTH: 17
; TYPE: PRT

; ORGANISM: Rattus norvegicus
US-10-499-762-17

Query Match 80.9%; Score 55; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| ||| |||
Db 1 CFGGRIDRIGAOSGLGC 17

RESULT 37

US-10-499-762-18
; Sequence 18, Application US/10499762
; Publication No. US20050143562A1
; GENERAL INFORMATION:
; APPLICANT: PHENOGENE THERAPEUTICS INC.
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFATY, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 09680.0252USWO
; CURRENT APPLICATION NUMBER: US/10/499,762
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/IB02/05778
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-499-762-18

Query Match 80.9%; Score 55; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| ||| |||
Db 1 CFGQXIDRIGAVSRLGC 17

RESULT 38

US-10-499-762-19
; Sequence 19, Application US/10499762
; Publication No. US20050143562A1
; GENERAL INFORMATION:
; APPLICANT: PHENOGENE THERAPEUTICS INC.
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFATY, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 09680.0252USWO
; CURRENT APPLICATION NUMBER: US/10/499,762
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/IB02/05778
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 19
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-499-762-19

Query Match 80.9%; Score 55; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17

Db 1 CFGKLDRIQSMGSLGC 17

RESULT 39

US-11-066-697-474
; Sequence 474, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 474
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-066-697-474

Query Match 80.9%; Score 55; DB 6; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17

Db 1 CFGGRMDRIGAQSGSLGC 17

RESULT 40

US-09-902-517-32
; Sequence 32, Application US/09902517
; Publication No. US20030109430A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14

; PRIOR APPLICATION NUMBER: 07/200,383

; PRIOR FILING DATE: 1988-05-31

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 32

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:
; OTHER INFORMATION: Amino acids encoding pBNP

US-09-902-517-32

Query Match 80.9%; Score 55; DB 3; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17

Db 3 CFGGRMDRIGAQSGSLGC 19

RESULT 41

US-09-902-517-34
; Sequence 34, Application US/09902517
; Publication No. US20030109430A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amino acids encoding pBNP
; US-09-902-517-34

Query Match 80.9%; Score 55; DB 3; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17

Db 3 CFGRRLDRIQSLGSLGC 19

RESULT 42

US-10-402-021-32
; Sequence 32, Application US/10402021
; Publication No. US20040002458A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John

APPLICANT: Scarborough, Robert M.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING NATRIURETIC PEPTIDE
TITLE OF INVENTION: (AMENDED)
FILE REFERENCE: 21902025203
CURRENT APPLICATION NUMBER: US/10/402,021
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: 09/287,892
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 07/477,226
PRIOR FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR FILING DATE: 1989-01-19
PRIOR APPLICATION NUMBER: 07/206,470
PRIOR FILING DATE: 1988-06-14
PRIOR APPLICATION NUMBER: 07/200,383
PRIOR FILING DATE: 1988-05-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Amino acids encoding pBNP
US-10-402-021-32

Query Match 80.9%; Score 55; DB 4; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
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Db 3 CFGGRMDRIGAGSLGC 19

RESULT 43
US-10-402-021-34
Sequence 34, Application US/10402021
Publication No. US20040002458A1
GENERAL INFORMATION:
APPLICANT: Selthamer, Jeffrey J.
APPLICANT: Lewicki, John
APPLICANT: Scarborough, Robert M.
APPLICANT: Porter, Gordon J.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING NATRIURETIC PEPTIDE
TITLE OF INVENTION: (AMENDED)
FILE REFERENCE: 219002025203
CURRENT APPLICATION NUMBER: US/10/402,021
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: 09/287,892
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 07/477,226
PRIOR FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR FILING DATE: 1989-01-19
PRIOR APPLICATION NUMBER: 07/206,470
PRIOR FILING DATE: 1988-06-14
PRIOR APPLICATION NUMBER: 07/200,383
PRIOR FILING DATE: 1988-05-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Amino acids encoding pBNP
US-10-402-021-34

Query Match 80.9%; Score 55; DB 4; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
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Db 3 CFGRRLDRIAGSLGC 19

RESULT 44
US-11-066-697-483
Sequence 483, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 483
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-483

Query Match 80.9%; Score 55; DB 6; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00058;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
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Db 3 CFGGRIDRIGAGSLGC 19

RESULT 45
US-09-752-724-3
Sequence 3, Application US/09752724
Patent No. US20010027181A1
GENERAL INFORMATION:
APPLICANT: KITAKAZE, Masafumi
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
TITLE OF INVENTION: ISCHEMIC HEART DISEASE
FILE REFERENCE: PP/S-38-252US
CURRENT APPLICATION NUMBER: US/09/752,724
CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: JP 98134/2000
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 22
TYPE: PRT
ORGANISM: frog
US-09-752-724-3

Query Match 80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
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Db 1 CFGGRMDRIGAQSGLGC 17

RESULT 46

US-09-752-724-9
; Sequence 9, Application US/09752724
; Patent No. US20010027181A1

; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; FILE REFERENCE: FP/S-38-252US
; CURRENT APPLICATION NUMBER: US/09/752,724
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens, porcine, rat
US-09-752-724-9

Query Match 80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
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Db 6 CFGKLDRIGSMSGLGC 22

RESULT 47

US-09-752-724-10
; Sequence 10, Application US/09752724
; Patent No. US20010027181A1

; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; FILE REFERENCE: FP/S-38-252US
; CURRENT APPLICATION NUMBER: US/09/752,724
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: PRT
; ORGANISM: chicken
US-09-752-724-10

Query Match 80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| | ||
Db 6 CFGVKLDRIGSMSGLGC 22

RESULT 48

US-09-752-724-11
; Sequence 11, Application US/09752724
; Patent No. US20010027181A1

; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; FILE REFERENCE: FP/S-38-252US
; CURRENT APPLICATION NUMBER: US/09/752,724
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 22
; TYPE: PRT
; ORGANISM: frog
US-09-752-724-11

Query Match 80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
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Db 6 CFGVKLDRIGAFAQSGLGC 22

RESULT 49

US-09-466-268B-9
; Sequence 9, Application US/09466268B
; Publication No. US20020082219A1

; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US1
; CURRENT APPLICATION NUMBER: US/09/466,268B
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-268B-9

Query Match 80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
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Db 6 CFGKLDRIGSMSGLGC 22

RESULT 50

US-09-912-425-3
; Sequence 3, Application US/09912425
; Patent No. US20020128176A1

; GENERAL INFORMATION:
; APPLICANT: Forssmann, Wolf-Georg
; APPLICANT: Maegert, Hans-Ulrich
; APPLICANT: Stief, Christian
; APPLICANT: Kuethe, Andrea
; APPLICANT: Deckert, Stefan
; APPLICANT: Becker, Armin
; APPLICANT: Jonas, Udo
; TITLE OF INVENTION: Treatment of Erectile Dysfunctions with C-Type
; TITLE OF INVENTION: Natriuretic Polypeptide (CNP) as a Monotherapy or in
; FILE REFERENCE: 011634us
; CURRENT APPLICATION NUMBER: US/09/912,425
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: DE19903087.1

; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-425-3

Query Match 80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. NO. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
||| ||| |||
Db 6 CFGKLDRI GSMGLGC 22

Search completed: January 26, 2006, 14:47:16
Job time : 67 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:43:48 ; Search time 7 Seconds
(without alignments)
26.299 Million cell updates/sec

Title: US-10-664-605-5
Perfect score: 68
Sequence: 1 CFGXXXDRIGXXSXGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA New: *
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep: *
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	80.9	28	7	US-11-112-277-16
2	55	80.9	28	7	US-11-112-277-50
3	55	80.9	28	7	US-11-112-277-51
4	55	80.9	28	7	US-11-059-814-4
5	55	80.9	28	7	US-11-175-690-309
6	55	80.9	121	6	US-10-510-880-3
7	55	80.9	126	6	US-10-977-334-5
8	55	80.9	131	6	US-10-510-880-2
9	55	80.9	151	7	US-11-059-814-7
10	55	80.9	152	7	US-11-059-814-16
11	55	80.9	153	6	US-10-977-334-4
12	55	80.9	637	7	US-11-175-690-222
13	50	73.5	26	7	US-11-175-690-321
14	50	73.5	27	7	US-11-175-690-322
15	50	73.5	27	7	US-11-175-690-323
16	50	73.5	28	7	US-11-175-690-323
17	50	73.5	28	7	US-11-175-690-369
18	50	73.5	29	7	US-11-175-690-314
19	50	73.5	29	7	US-11-175-690-315
20	50	73.5	32	6	US-10-510-880-4
21	50	73.5	32	6	US-10-977-334-3
22	50	73.5	32	7	US-11-043-590-17
23	50	73.5	32	7	US-11-175-690-288
24	50	73.5	32	7	US-11-175-690-298
25	50	73.5	32	7	US-11-175-690-304

26	50	73.5	32	7	US-11-175-690-317	Sequence 317, App
27	50	73.5	32	7	US-11-175-690-318	Sequence 318, App
28	50	73.5	32	7	US-11-175-690-370	Sequence 370, App
29	50	73.5	42	7	US-11-043-590-15	Sequence 15, Appli
30	50	73.5	52	7	US-11-175-690-368	Sequence 368, App
31	50	73.5	60	7	US-11-043-590-16	Sequence 16, Appli
32	50	73.5	108	6	US-10-510-880-5	Sequence 5, Appli
33	50	73.5	108	6	US-10-875-800-1	Sequence 1, Appli
34	50	73.5	108	6	US-10-299-977-1	Sequence 1, Appli
35	50	73.5	134	6	US-10-510-880-1	Sequence 1, Appli
36	50	73.5	134	6	US-10-875-800-2	Sequence 2, Appli
37	50	73.5	134	7	US-11-043-590-12	Sequence 12, Appli
38	50	73.5	162	7	US-11-043-590-13	Sequence 13, Appli
39	50	73.5	630	7	US-11-175-690-234	Sequence 234, App
40	50	73.5	631	7	US-11-175-690-235	Sequence 235, App
41	50	73.5	632	7	US-11-175-690-236	Sequence 236, App
42	50	73.5	633	7	US-11-175-690-228	Sequence 228, App
43	50	73.5	641	7	US-11-175-690-211	Sequence 211, App
44	50	73.5	641	7	US-11-175-690-230	Sequence 230, App
45	50	73.5	661	7	US-11-175-690-281	Sequence 281, App
46	50	73.5	663	7	US-11-175-690-284	Sequence 284, App
47	50	73.5	665	7	US-11-175-690-282	Sequence 282, App
48	50	73.5	667	7	US-11-175-690-227	Sequence 227, App
49	50	73.5	670	7	US-11-175-690-283	Sequence 283, App
50	50	73.5	673	7	US-11-175-690-201	Sequence 201, App
51	50	73.5	673	7	US-11-175-690-217	Sequence 217, App
52	50	73.5	673	7	US-11-175-690-231	Sequence 231, App
53	32	47.1	91	6	US-10-485-788A-818	Sequence 818, App
54	32	47.1	91	7	US-11-053-076-203	Sequence 203, App
55	31	45.6	770	7	US-11-024-959-358	Sequence 358, App
56	31	45.6	2221	7	US-11-126-313-30	Sequence 30, Appli
57	30	44.1	32	6	US-10-512-325-5	Sequence 5, Appli
58	30	44.1	32	7	US-11-196-919-4	Sequence 4, Appli
59	30	44.1	418	6	US-10-512-325-3	Sequence 3, Appli
60	30	44.1	418	7	US-11-196-919-2	Sequence 2, Appli
61	30	44.1	487	6	US-10-055-877-268	Sequence 268, App
62	30	44.1	556	6	US-10-055-877-81	Sequence 81, Appli
63	30	44.1	573	6	US-10-055-877-79	Sequence 79, Appli
64	30	44.1	833	7	US-11-076-187-5	Sequence 5, Appli
65	30	44.1	1176	6	US-10-821-234-897	Sequence 897, App
66	29	42.6	85	6	US-10-467-657-3010	Sequence 3010, Ap
67	29	42.6	347	6	US-10-055-877-269	Sequence 269, App
68	29	42.6	347	6	US-10-055-877-270	Sequence 270, App
69	29	42.6	347	6	US-10-055-877-271	Sequence 271, App
70	29	42.6	550	6	US-10-055-877-274	Sequence 274, App
71	29	42.6	550	6	US-10-055-877-275	Sequence 275, App
72	29	42.6	551	6	US-10-055-877-276	Sequence 276, App
73	29	42.6	551	6	US-10-055-877-277	Sequence 277, App
74	28	41.2	273	7	US-11-070-080-19	Sequence 19, Appli
75	28	41.2	349	7	US-11-108-528-44	Sequence 44, Appli
76	28	41.2	349	7	US-11-108-528-46	Sequence 46, Appli
77	28	41.2	381	6	US-10-641-678-74	Sequence 74, Appli
78	28	41.2	412	6	US-10-878-556A-149	Sequence 149, App
79	28	41.2	644	6	US-10-467-657-5958	Sequence 5958, Ap
80	28	41.2	886	6	US-10-821-234-1329	Sequence 1329, Ap
81	27	39.7	185	6	US-10-467-657-1228	Sequence 1228, Ap
82	27	39.7	284	6	US-10-714-887-102	Sequence 102, App
83	27	39.7	341	6	US-10-467-657-5408	Sequence 5408, Ap
84	27	39.7	382	7	US-11-000-463-447	Sequence 447, App
85	27	39.7	412	7	US-11-117-161-11	Sequence 11, Appli
86	27	39.7	412	7	US-11-080-257-11	Sequence 11, Appli
87	27	39.7	445	6	US-10-858-730-4	Sequence 4, Appli
88	27	39.7	579	7	US-10-467-657-2946	Sequence 2946, Ap
89	26	38.2	66	6	US-10-714-887-68	Sequence 68, Appli
90	26	38.2	168	6	US-10-653-343-23	Sequence 23, Appli
91	26	38.2	221	7	US-10-763-712A-115	Sequence 115, App
92	26	38.2	236	6	US-10-714-887-124	Sequence 124, App
93	26	38.2	238	6	US-10-170-997-2	Sequence 2, Appli
94	26	38.2	255	6	US-10-170-997-2	Sequence 2, Appli
95	26	38.2	255	7	US-11-182-946-11	Sequence 11, Appli
96	26	38.2	259	6	US-10-631-558-4	Sequence 4, Appli
97	26	38.2	259	6	US-10-631-558-4	Sequence 4, Appli
98	26	38.2	300	7	US-11-006-119-31	Sequence 31, Appli

99	26	38.2	329	6	US-10-714-887-116	Sequence 116, App
100	26	38.2	343	7	US-11-074-176-160	Sequence 160, App
101	26	38.2	359	6	US-10-055-877-272	Sequence 272, App
102	26	38.2	361	6	US-10-467-657-7946	Sequence 7946, Ap
103	26	38.2	362	6	US-10-858-730-123	Sequence 123, App
104	26	38.2	394	6	US-10-392-234A-46	Sequence 46, Appl
105	26	38.2	394	6	US-10-392-234A-52	Sequence 52, Appl
106	26	38.2	412	7	US-11-117-161-13	Sequence 13, Appl
107	26	38.2	412	7	US-11-080-257-13	Sequence 13, Appl
108	26	38.2	416	7	US-11-016-706-38	Sequence 38, Appl
109	26	38.2	464	7	US-11-024-959-488	Sequence 488, App
110	26	38.2	504	7	US-11-087-100-32	Sequence 32, Appl
111	26	38.2	504	7	US-11-087-084-32	Sequence 32, Appl
112	26	38.2	504	7	US-11-087-085-32	Sequence 26, Appl
113	26	38.2	510	7	US-11-087-100-26	Sequence 26, Appl
114	26	38.2	510	7	US-11-087-084-26	Sequence 26, Appl
115	26	38.2	510	7	US-11-087-085-26	Sequence 26, Appl
116	26	38.2	516	6	US-10-486-968-52	Sequence 52, Appl
117	26	38.2	544	6	US-10-980-388-40	Sequence 40, Appl
118	26	38.2	592	6	US-10-467-657-4888	Sequence 4888, Ap
119	26	38.2	642	6	US-10-995-561-631	Sequence 631, App
120	26	38.2	657	6	US-10-995-561-622	Sequence 622, App
121	26	38.2	792	7	US-11-108-172-1127	Sequence 1127, Ap
122	26	38.2	984	6	US-10-995-561-629	Sequence 629, App
123	26	38.2	1076	6	US-10-467-657-5708	Sequence 5708, Ap
124	26	38.2	1389	6	US-10-467-657-334	Sequence 334, App
125	26	38.2	1503	7	US-11-087-100-6	Sequence 6, Appli
126	26	38.2	1503	7	US-11-087-084-6	Sequence 6, Appli
127	26	38.2	1503	7	US-11-087-085-6	Sequence 6, Appli
128	26	38.2	1713	6	US-10-766-317-2	Sequence 2, Appli
129	26	38.2	2059	7	US-10-766-317-6	Sequence 6, Appli
130	26	38.2	2059	7	US-11-087-100-4	Sequence 4, Appli
131	26	38.2	2059	7	US-11-087-084-4	Sequence 4, Appli
132	26	38.2	2059	7	US-11-087-085-4	Sequence 4, Appli
133	26	38.2	2296	6	US-10-995-561-633	Sequence 633, App
134	26	38.2	2355	6	US-10-995-561-623	Sequence 623, App
135	26	38.2	2355	6	US-10-995-561-627	Sequence 627, App
136	26	38.2	2384	6	US-10-821-234-1545	Sequence 1545, Ap
137	26	38.2	2386	6	US-10-995-561-626	Sequence 626, App
138	26	38.2	3303	6	US-10-766-317-4	Sequence 4, Appli
139	26	38.2	3507	7	US-11-075-185-7	Sequence 7, Appli
140	26	38.2	3712	7	US-11-019-711-48	Sequence 48, Appl
141	26	38.2	3712	7	US-11-019-711-51	Sequence 51, Appl
142	25	37.5	815	7	US-11-073-112-3	Sequence 3, Appli
143	25	36.8	15	7	US-11-033-039-629	Sequence 629, App
144	25	36.8	31	7	US-11-033-039-631	Sequence 631, App
145	25	36.8	45	6	US-10-957-887B-41	Sequence 41, Appl
146	25	36.8	120	7	US-11-116-144-160	Sequence 160, App
147	25	36.8	120	7	US-11-116-144-161	Sequence 161, App
148	25	36.8	169	6	US-10-878-556A-81	Sequence 81, Appl
149	25	36.8	169	5	US-09-978-360A-443	Sequence 443, App
150	25	36.8	171	6	US-10-467-657-1838	Sequence 1838, Ap
151	25	36.8	178	6	US-10-821-234-1647	Sequence 1647, Ap
152	25	36.8	188	6	US-10-467-657-1982	Sequence 1982, Ap
153	25	36.8	210	6	US-10-467-657-3984	Sequence 3984, Ap
154	25	36.8	210	6	US-10-055-877-24	Sequence 24, Appl
155	25	36.8	218	7	US-11-082-389-318	Sequence 318, App
156	25	36.8	234	6	US-10-467-657-7422	Sequence 7422, Ap
157	25	36.8	236	7	US-11-000-463-278	Sequence 278, App
158	25	36.8	251	6	US-10-821-234-1470	Sequence 1470, Ap
159	25	36.8	301	6	US-10-512-184-37	Sequence 37, Appl
160	25	36.8	311	7	US-11-082-389-168	Sequence 168, App
161	25	36.8	316	6	US-10-467-657-4040	Sequence 4040, Ap
162	25	36.8	321	6	US-10-478-345-8	Sequence 8, Appli
163	25	36.8	322	6	US-10-055-877-26	Sequence 26, Appl
164	25	36.8	325	6	US-10-063-703-64	Sequence 64, Appl
165	25	36.8	325	7	US-11-102-240-64	Sequence 64, Appl
166	25	36.8	335	7	US-11-152-892-12	Sequence 12, Appl
167	25	36.8	344	7	US-11-083-800-10	Sequence 10, Appl
168	25	36.8	361	7	US-11-120-308-82	Sequence 82, Appl
169	25	36.8	369	6	US-10-793-626-672	Sequence 672, App
170	25	36.8	374	6	US-10-055-877-20	Sequence 20, Appl
171	25	36.8	374	6	US-10-055-877-22	Sequence 22, Appl
172	25	36.8	374	7	US-11-037-243-61	Sequence 61, Appl
173	25	36.8	382	7	US-11-134-795-19	Sequence 19, Appl
174	25	36.8	396	7	US-11-114-922-76	Sequence 76, Appl
175	25	36.8	398	6	US-10-467-657-5642	Sequence 5642, Ap
176	25	36.8	401	6	US-10-878-556A-179	Sequence 179, App
177	25	36.8	405	6	US-10-467-657-2310	Sequence 2310, Ap
178	25	36.8	423	6	US-10-467-657-6536	Sequence 6536, Ap
179	25	36.8	427	6	US-10-714-887-122	Sequence 122, App
180	25	36.8	433	7	US-11-082-389-332	Sequence 332, App
181	25	36.8	446	7	US-11-082-389-316	Sequence 316, App
182	25	36.8	447	6	US-10-967-527A-14	Sequence 14, Appl
183	25	36.8	448	6	US-10-967-527A-16	Sequence 16, Appl
184	25	36.8	449	6	US-10-821-234-1089	Sequence 1089, Ap
185	25	36.8	460	6	US-10-467-657-3136	Sequence 3136, Ap
186	25	36.8	467	7	US-11-082-389-334	Sequence 334, App
187	25	36.8	472	7	US-11-165-211-1	Sequence 1, Appli
188	25	36.8	472	7	US-11-165-211-2	Sequence 2, Appli
189	25	36.8	472	7	US-11-165-211-3	Sequence 3, Appli
190	25	36.8	472	7	US-11-165-211-4	Sequence 4, Appli
191	25	36.8	472	7	US-11-165-211-5	Sequence 5, Appli
192	25	36.8	472	7	US-11-165-211-7	Sequence 7, Appli
193	25	36.8	472	7	US-11-165-226-1	Sequence 1, Appli
194	25	36.8	472	7	US-11-165-226-2	Sequence 2, Appli
195	25	36.8	472	7	US-11-165-226-3	Sequence 3, Appli
196	25	36.8	472	7	US-11-165-226-4	Sequence 4, Appli
197	25	36.8	472	7	US-11-165-226-5	Sequence 5, Appli
198	25	36.8	472	7	US-11-165-226-7	Sequence 7, Appli
199	25	36.8	472	7	US-11-165-226-9	Sequence 9, Appli
200	25	36.8	472	7	US-11-165-226-10	Sequence 10, Appl
201	25	36.8	472	7	US-11-165-226-11	Sequence 11, Appl
202	25	36.8	472	7	US-11-165-226-12	Sequence 12, Appl
203	25	36.8	472	7	US-11-165-226-13	Sequence 13, Appl
204	25	36.8	494	6	US-10-467-657-4376	Sequence 4376, Ap
205	25	36.8	539	6	US-10-467-657-6792	Sequence 6792, Ap
206	25	36.8	567	6	US-10-512-184-254	Sequence 254, App
207	25	36.8	569	6	US-10-512-184-66	Sequence 66, Appl
208	25	36.8	576	6	US-10-512-184-65	Sequence 65, Appl
209	25	36.8	594	6	US-10-467-657-6376	Sequence 6376, Ap
210	25	36.8	607	7	US-11-024-959-381	Sequence 381, App
211	25	36.8	615	6	US-10-512-184-50	Sequence 50, Appl
212	25	36.8	618	6	US-10-512-184-48	Sequence 48, Appl
213	25	36.8	625	6	US-10-512-184-47	Sequence 47, Appl
214	25	36.8	626	6	US-10-512-184-49	Sequence 49, Appl
215	25	36.8	645	7	US-11-154-337-13	Sequence 13, Appl
216	25	36.8	742	7	US-11-127-877-43	Sequence 43, Appl
217	25	36.8	765	6	US-10-821-234-1164	Sequence 1164, Ap
218	25	36.8	1144	6	US-10-467-962B-89	Sequence 89, Appl
219	25	36.8	1255	6	US-10-770-726-62	Sequence 62, Appl
220	25	36.8	1255	7	US-11-022-562-213	Sequence 213, App
221	25	36.8	1255	7	US-11-113-202-10	Sequence 10, Appl
222	25	36.8	1255	7	US-11-033-039-553	Sequence 553, App
223	25	36.8	1255	7	US-11-155-288-9	Sequence 9, Appli
224	25	36.8	1255	7	US-11-202-516-4	Sequence 4, Appli
225	25	36.8	1258	7	US-11-033-039-930	Sequence 930, App
226	25	36.8	2440	6	US-10-766-317-10	Sequence 10, Appl
227	25	36.8	2471	7	US-11-050-346-68	Sequence 68, Appl
228	25	36.8	2556	7	US-11-156-843-94	Sequence 94, Appl
229	25	36.8	3500	7	US-11-050-346-67	Sequence 67, Appl
230	25	36.8	3635	7	US-11-085-775-2	Sequence 2, Appli
231	24	36.0	163	6	US-10-467-657-5884	Sequence 47, Appl
232	24	35.3	30	7	US-11-156-843-56	Sequence 56, Appl
233	24	35.3	30	7	US-11-156-843-97	Sequence 94, Appl
234	24	35.3	30	7	US-11-156-843-98	Sequence 97, Appl
235	24	35.3	30	7	US-11-156-843-98	Sequence 98, Appl
236	24	35.3	49	6	US-10-467-657-4058	Sequence 4058, Ap
237	24	35.3	75	6	US-10-467-657-9139	Sequence 9139, Ap
238	24	35.3	79	7	US-11-077-386-21	Sequence 21, Appl
239	24	35.3	124	6	US-10-467-657-3838	Sequence 3838, Ap
240	24	35.3	142	6	US-10-763-712A-117	Sequence 117, App
241	24	35.3	187	7	US-11-205-109-19	Sequence 19, Appl
242	24	35.3	201	6	US-10-467-657-2006	Sequence 2006, Ap
243	24	35.3	217	6	US-10-467-657-8174	Sequence 8174, Ap
244	24	35.3	220	6	US-10-467-657-8734	Sequence 8734, Ap

245	24	35.3	220	6	US-10-714-887-60	Sequence 60, Appl	318	24	35.3	2551	6	US-10-453-372-256	Sequence 256, App
246	24	35.3	225	6	US-10-467-657-146	Sequence 146, App	319	24	35.3	2551	7	US-11-128-059-96	Sequence 96, Appl
247	24	35.3	225	6	US-10-467-657-4138	Sequence 4138, Ap	320	24	35.3	2766	6	US-10-877-346-62	Sequence 62, Appl
248	24	35.3	225	6	US-10-467-657-7072	Sequence 7072, Ap	321	24	35.3	5179	7	US-11-108-172-1068	Sequence 1068, Ap
249	24	35.3	225	6	US-10-714-887-112	Sequence 112, App	322	23.5	34.6	249	7	US-11-054-515-1957	Sequence 1957, Ap
250	24	35.3	242	6	US-10-714-887-66	Sequence 66, Appl	323	23	33.8	21	6	US-10-893-584-205	Sequence 205, App
251	24	35.3	254	6	US-10-467-657-3450	Sequence 3450, Ap	324	23	33.8	24	6	US-10-467-657-9084	Sequence 9084, Ap
252	24	35.3	279	6	US-10-055-877-197	Sequence 197, App	325	23	33.8	83	7	US-11-082-389-158	Sequence 158, App
253	24	35.3	279	6	US-10-714-887-58	Sequence 58, Appl	326	23	33.8	85	6	US-10-467-657-7438	Sequence 7438, Ap
254	24	35.3	284	6	US-10-467-657-536	Sequence 536, App	327	23	33.8	86	6	US-10-485-788A-822	Sequence 822, App
255	24	35.3	297	6	US-10-510-386-16	Sequence 16, Appl	328	23	33.8	86	7	US-11-053-076-207	Sequence 207, App
256	24	35.3	312	6	US-10-714-887-44	Sequence 44, Appl	329	23	33.8	89	6	US-10-467-657-3582	Sequence 3582, Ap
257	24	35.3	323	7	US-11-120-308-108	Sequence 108, App	330	23	33.8	110	6	US-10-793-626-930	Sequence 930, App
258	24	35.3	323	7	US-11-120-308-116	Sequence 116, App	331	23	33.8	119	6	US-10-467-657-6838	Sequence 6838, App
259	24	35.3	339	6	US-10-467-657-4318	Sequence 4318, Ap	332	23	33.8	122	7	US-11-116-144-164	Sequence 164, App
260	24	35.3	360	7	US-11-108-528-8	Sequence 8, Appli	333	23	33.8	133	6	US-10-793-626-2072	Sequence 2072, Ap
261	24	35.3	363	7	US-11-111-239-6	Sequence 6, Appli	334	23	33.8	160	7	US-11-044-285-4	Sequence 4, Appli1
262	24	35.3	386	6	US-10-858-730-236	Sequence 236, App	335	23	33.8	163	6	US-10-467-657-4786	Sequence 4786, Ap
263	24	35.3	393	7	US-11-111-239-8	Sequence 8, Appl1	336	23	33.8	181	6	US-10-793-626-560	Sequence 560, App
264	24	35.3	396	6	US-10-510-386-238	Sequence 238, App	337	23	33.8	199	6	US-10-793-626-2932	Sequence 2932, Ap
265	24	35.3	399	6	US-10-510-386-30	Sequence 30, Appl	338	23	33.8	221	6	US-10-467-657-5140	Sequence 1139, Ap
266	24	35.3	400	6	US-11-111-239-10	Sequence 10, Appl	339	23	33.8	223	6	US-10-821-234-1139	Sequence 5140, Ap
267	24	35.3	400	7	US-10-467-657-7588	Sequence 7588, Ap	340	23	33.8	224	7	US-11-000-463-279	Sequence 279, App
268	24	35.3	400	7	US-11-120-308-114	Sequence 114, App	341	23	33.8	226	7	US-11-151-601-29	Sequence 29, Appl
269	24	35.3	410	6	US-10-995-561-969	Sequence 18, Appl	342	23	33.8	226	7	US-11-151-601-37	Sequence 37, Appl
270	24	35.3	413	7	US-11-043-889-18	Sequence 196, App	343	23	33.8	229	6	US-10-131-826A-178	Sequence 178, App
271	24	35.3	417	6	US-10-793-626-196	Sequence 18, Appl	344	23	33.8	230	6	US-10-467-657-9008	Sequence 9008, Ap
272	24	35.3	427	7	US-11-110-851-66	Sequence 66, Appl	345	23	33.8	238	6	US-10-467-657-4954	Sequence 4954, Ap
273	24	35.3	436	6	US-10-517-939-10	Sequence 10, Appl	346	23	33.8	240	7	US-11-212-443-139	Sequence 139, App
274	24	35.3	436	7	US-11-043-889-58	Sequence 58, Appl	347	23	33.8	241	6	US-10-467-657-1400	Sequence 1400, Ap
275	24	35.3	437	7	US-11-043-889-55	Sequence 55, Appl	348	23	33.8	243	6	US-10-714-887-50	Sequence 50, Appl
276	24	35.3	447	7	US-11-124-368A-185	Sequence 185, App	349	23	33.8	243	7	US-11-129-104-91	Sequence 91, Appl
277	24	35.3	449	6	US-10-878-556A-57	Sequence 57, Appl	350	23	33.8	271	6	US-10-714-887-48	Sequence 48, Appl
278	24	35.3	455	6	US-10-467-657-5828	Sequence 5828, Ap	351	23	33.8	278	6	US-10-467-657-1848	Sequence 1848, Ap
279	24	35.3	465	6	US-10-467-657-5040	Sequence 5040, Ap	352	23	33.8	301	6	US-10-793-626-1396	Sequence 1396, Ap
280	24	35.3	484	7	US-11-147-725-2	Sequence 2, Appli	353	23	33.8	302	6	US-10-793-626-2170	Sequence 2170, Ap
281	24	35.3	505	6	US-10-793-626-2220	Sequence 2220, Ap	354	23	33.8	312	7	US-11-054-281-32	Sequence 32, Appl
282	24	35.3	514	6	US-10-957-569-48	Sequence 48, Appl	355	23	33.8	312	7	US-11-054-281-320	Sequence 320, App
283	24	35.3	516	6	US-10-995-561-559	Sequence 559, App	356	23	33.8	312	7	US-11-054-281-324	Sequence 324, App
284	24	35.3	533	7	US-11-128-059-58	Sequence 58, Appl	357	23	33.8	318	7	US-11-109-156-15	Sequence 15, Appl
285	24	35.3	554	7	US-11-159-902-4	Sequence 4, Appli	358	23	33.8	318	7	US-11-111-239-2	Sequence 2, Appli1
286	24	35.3	556	6	US-10-063-703-24	Sequence 24, Appl	359	23	33.8	321	6	US-10-467-657-2504	Sequence 2504, Ap
287	24	35.3	556	7	US-11-102-240-24	Sequence 24, Appl	360	23	33.8	330	7	US-11-152-892-10	Sequence 10, Appl
288	24	35.3	557	6	US-10-512-109-9	Sequence 9, Appli	361	23	33.8	333	6	US-10-878-556A-174	Sequence 174, App
289	24	35.3	558	6	US-10-512-109-11	Sequence 11, Appl	362	23	33.8	338	6	US-10-467-657-3178	Sequence 3178, Ap
290	24	35.3	585	7	US-11-012-762-6	Sequence 6, Appli	363	23	33.8	340	6	US-10-055-877-69	Sequence 69, Appl
291	24	35.3	613	6	US-10-517-939-298	Sequence 298, App	364	23	33.8	344	7	US-11-052-554A-43	Sequence 43, Appl
292	24	35.3	651	7	US-11-124-368A-184	Sequence 184, App	365	23	33.8	354	6	US-10-467-657-7260	Sequence 7260, Ap
293	24	35.3	702	6	US-10-467-657-8280	Sequence 8280, Ap	366	23	33.8	357	7	US-11-165-466-2	Sequence 2, Appli
294	24	35.3	770	7	US-11-070-627-8	Sequence 8, Appli	367	23	33.8	357	7	US-11-165-466-2	Sequence 2, Appli1
295	24	35.3	770	7	US-11-070-627-10	Sequence 10, Appl	368	23	33.8	359	7	US-11-108-528-32	Sequence 32, Appl
296	24	35.3	774	7	US-11-070-627-7	Sequence 7, Appli	369	23	33.8	360	7	US-11-108-528-6	Sequence 6, Appli
297	24	35.3	833	7	US-11-159-902-2	Sequence 2, Appli	370	23	33.8	361	7	US-11-052-554A-169	Sequence 169, App
298	24	35.3	884	6	US-10-995-561-786	Sequence 786, App	371	23	33.8	363	7	US-11-054-281-120	Sequence 120, App
299	24	35.3	911	6	US-10-858-730-9	Sequence 9, Appli	372	23	33.8	365	6	US-10-624-932-24	Sequence 24, Appl
300	24	35.3	921	7	US-11-183-624-2	Sequence 2, Appli	373	23	33.8	372	7	US-11-108-528-10	Sequence 10, Appl
301	24	35.3	1023	6	US-10-995-561-968	Sequence 968, App	374	23	33.8	372	7	US-11-108-528-34	Sequence 34, Appl
302	24	35.3	1076	6	US-10-131-826A-219	Sequence 219, App	375	23	33.8	377	6	US-10-467-657-7508	Sequence 7508, Ap
303	24	35.3	1125	7	US-11-024-959-360	Sequence 360, App	376	23	33.8	380	6	US-10-624-932-20	Sequence 20, Appl
304	24	35.3	1416	7	US-11-128-059-60	Sequence 60, Appl	377	23	33.8	380	6	US-10-624-932-22	Sequence 22, Appl
305	24	35.3	1494	7	US-11-128-059-78	Sequence 78, Appl	378	23	33.8	380	7	US-11-108-528-28	Sequence 28, Appl
306	24	35.3	1532	6	US-10-821-234-914	Sequence 914, App	379	23	33.8	380	7	US-11-108-528-30	Sequence 30, Appl
307	24	35.3	1765	6	US-10-055-877-140	Sequence 140, App	380	23	33.8	384	6	US-10-467-657-5664	Sequence 5664, Ap
308	24	35.3	1940	6	US-10-055-877-141	Sequence 141, App	381	23	33.8	384	6	US-11-129-143-77	Sequence 77, Appl
309	24	35.3	2086	7	US-11-128-059-82	Sequence 82, Appl	382	23	33.8	389	6	US-10-821-234-1401	Sequence 1401, Ap
310	24	35.3	2098	6	US-10-055-877-253	Sequence 253, App	383	23	33.8	389	7	US-11-108-528-14	Sequence 14, Appl
311	24	35.3	2313	7	US-11-128-059-80	Sequence 80, Appl	384	23	33.8	391	7	US-11-108-528-12	Sequence 12, Appl
312	24	35.3	2358	7	US-11-128-059-74	Sequence 74, Appl	385	23	33.8	413	7	US-11-052-554A-308	Sequence 308, App
313	24	35.3	2417	6	US-10-453-372-228	Sequence 228, App	386	23	33.8	425	6	US-10-858-730-3	Sequence 3, Appli
314	24	35.3	2439	7	US-11-128-059-76	Sequence 76, Appl	387	23	33.8	435	6	US-10-467-657-4570	Sequence 4570, Ap
315	24	35.3	2458	7	US-11-128-059-94	Sequence 94, Appl	388	23	33.8	473	7	US-11-040-595-9	Sequence 9, Appli
316	24	35.3	2491	6	US-10-995-561-769	Sequence 769, App	389	23	33.8	474	7	US-11-040-595-8	Sequence 8, Appli
317	24	35.3	2505	7	US-11-126-313-33	Sequence 33, Appl	390	23	33.8	480	7	US-11-080-991-76	Sequence 76, Appl

391	23	33.8	487	7	US-11-040-595-6	Sequence 6, Appli
392	23	33.8	490	6	US-10-131-826A-356	Sequence 356, App
393	23	33.8	494	7	US-11-165-697-48	Sequence 48, Appl
394	23	33.8	494	7	US-11-165-697-49	Sequence 49, Appl
395	23	33.8	500	7	US-11-120-308-138	Sequence 138, Appl
396	23	33.8	505	6	US-10-467-657-5148	Sequence 5148, Ap
397	23	33.8	508	6	US-10-467-657-7826	Sequence 7826, Ap
398	23	33.8	518	6	US-10-821-234-1165	Sequence 1165, Ap
399	23	33.8	525	6	US-10-763-712A-108	Sequence 108, App
400	23	33.8	525	7	US-11-082-389-36	Sequence 36, Appl
401	23	33.8	542	7	US-11-019-711-97	Sequence 97, Appl
402	23	33.8	545	7	US-11-082-389-34	Sequence 34, Appl
403	23	33.8	547	7	US-11-082-389-86	Sequence 86, Appl
404	23	33.8	550	6	US-10-878-556A-166	Sequence 166, App
405	23	33.8	560	7	US-11-205-109-38	Sequence 38, Appl
406	23	33.8	561	6	US-10-454-437-330	Sequence 330, App
407	23	33.8	575	6	US-10-980-388-46	Sequence 46, Appl
408	23	33.8	579	7	US-11-045-802-33	Sequence 33, Appl
409	23	33.8	601	6	US-10-467-657-7120	Sequence 7120, Ap
410	23	33.8	608	7	US-11-024-959-481	Sequence 481, App
411	23	33.8	611	7	US-11-082-389-436	Sequence 436, App
412	23	33.8	644	7	US-11-024-959-502	Sequence 502, App
413	23	33.8	655	7	US-11-184-860-1	Sequence 1, Appli
414	23	33.8	655	7	US-11-124-368A-296	Sequence 296, App
415	23	33.8	655	7	US-11-124-368A-297	Sequence 297, App
416	23	33.8	665	7	US-11-113-837-19	Sequence 19, Appl
417	23	33.8	709	7	US-11-165-067A-9	Sequence 9, Appli
418	23	33.8	717	6	US-10-467-657-8056	Sequence 8056, Ap
419	23	33.8	732	6	US-10-467-657-5888	Sequence 5888, Ap
420	23	33.8	879	6	US-10-858-730-10	Sequence 10, Appl
421	23	33.8	883	6	US-10-858-730-207	Sequence 207, App
422	23	33.8	897	6	US-10-336-263A-58	Sequence 58, Appl
423	23	33.8	914	7	US-11-052-554A-160	Sequence 160, App
424	23	33.8	930	6	US-10-821-234-1188	Sequence 1188, Ap
425	23	33.8	1059	6	US-10-336-263A-54	Sequence 54, Appl
426	23	33.8	1059	6	US-10-336-263A-56	Sequence 56, Appl
427	23	33.8	1210	7	US-11-108-172-692	Sequence 692, App
428	23	33.8	1236	6	US-10-873-528-109	Sequence 109, App
429	23	33.8	1403	6	US-10-055-877-52	Sequence 52, Appl
430	23	33.8	1404	6	US-10-453-372-878	Sequence 878, App
431	23	33.8	1404	6	US-10-055-877-44	Sequence 44, Appl
432	23	33.8	1404	6	US-10-453-372-870	Sequence 870, App
433	23	33.8	1547	6	US-10-453-372-886	Sequence 886, App
434	23	33.8	1548	7	US-11-108-172-1095	Sequence 1095, Ap
435	23	33.8	1577	6	US-10-055-877-54	Sequence 54, Appl
436	23	33.8	1577	6	US-10-453-372-882	Sequence 882, App
437	23	33.8	1577	6	US-10-453-372-884	Sequence 884, App
438	23	33.8	1618	6	US-10-984-645-2	Sequence 2, Appli
439	23	33.8	1620	6	US-10-453-372-868	Sequence 868, App
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444	23	33.8	1892	7	US-11-075-185-6	Sequence 6, Appli
445	23	33.8	1992	7	US-11-013-759-3	Sequence 3, Appli
446	23	33.8	1992	7	US-11-013-759-13	Sequence 13, Appl
447	23	33.8	2047	7	US-11-013-759-4	Sequence 4, Appli
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449	23	33.8	2314	7	US-11-013-759-11	Sequence 11, Appl
450	23	33.8	2890	7	US-11-115-639-31	Sequence 31, Appl
451	23	33.8	2890	7	US-11-115-639-32	Sequence 32, Appl
452	23	33.8	2890	7	US-11-115-639-33	Sequence 33, Appl
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455	23	33.8	3655	7	US-11-075-185-5	Sequence 5, Appli
456	23	33.8	3690	6	US-10-995-561-1016	Sequence 1016, Ap
457	23	33.8	3704	6	US-10-513-786-1	Sequence 1, Appli
458	23	33.8	3714	6	US-10-995-561-1015	Sequence 1015, Ap
459	23	33.8	3717	6	US-10-821-234-1076	Sequence 1076, Ap
460	23	33.8	8695	7	US-11-205-109-15	Sequence 15, Appl
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463	22	32.4	14	7	US-11-188-552-42	Sequence 42, Appl
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465	22	32.4	465	17	US-11-062-186-60	Sequence 60, Appl
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467	22	32.4	467	23	US-10-893-584-268	Sequence 268, App
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469	22	32.4	469	26	US-11-115-003-4	Sequence 254, App
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474	22	32.4	474	30	US-11-156-843-64	Sequence 67, Appl
475	22	32.4	475	30	US-11-156-843-73	Sequence 73, Appl
476	22	32.4	476	30	US-11-156-843-76	Sequence 76, Appl
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491	22	32.4	491	7	US-11-053-076-133	Sequence 133, App
492	22	32.4	492	7	US-11-075-351-59	Sequence 59, Appl
493	22	32.4	493	7	US-10-793-626-424	Sequence 11, Appl
494	22	32.4	494	113	US-10-793-626-424	Sequence 424, App
495	22	32.4	495	119	US-10-467-657-5374	Sequence 5374, App
496	22	32.4	496	138	US-10-467-657-5374	Sequence 117, App
497	22	32.4	497	140	US-11-054-281-117	Sequence 3170, Ap
498	22	32.4	498	153	US-10-793-626-3170	Sequence 4112, Ap
499	22	32.4	499	153	US-10-467-657-4112	Sequence 1720, Ap
500	22	32.4	500	157	US-10-793-626-1720	Sequence 352, App
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505	22	32.4	505	185	US-10-467-657-4092	Sequence 7068, Ap
506	22	32.4	506	185	US-10-467-657-7068	Sequence 9, Appli
507	22	32.4	507	185	US-10-923-022-9	Sequence 758, App
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509	22	32.4	509	6	US-10-923-022-8	Sequence 8, Appli
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515	22	32.4	515	191	US-10-467-657-818	Sequence 3, Appli
516	22	32.4	516	6	US-10-923-022-3	Sequence 7, Appli
517	22	32.4	517	6	US-10-923-022-7	Sequence 5, Appli
518	22	32.4	518	198	US-10-923-022-5	Sequence 246, App
519	22	32.4	519	200	US-10-454-437-246	Sequence 10, Appl
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521	22	32.4	521	203	US-10-467-657-3100	Sequence 4830, Ap
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523	22	32.4	523	7	US-11-165-067A-47	Sequence 7, Appli
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527	22	32.4	527	6	US-10-793-626-2780	Sequence 2780, Ap
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530	22	32.4	530	256	US-11-179-977-15	Sequence 113, App
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532	22	32.4	532	261	US-11-134-795-12	Sequence 144, App
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535	22	32.4	535	268	US-11-010-795-24	Sequence 1310, Ap
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543	22	32.4	307	6	US-10-467-657-7006	Sequence 7006, Ap	616	22	32.4	523	6	US-10-453-372-1006	Sequence 1006, Ap
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552	22	32.4	334	6	US-10-714-887-46	Sequence 46, Appli	625	22	32.4	619	7	US-11-109-157A-42	Sequence 42, Appli
553	22	32.4	334	7	US-11-111-239-4	Sequence 14, Appli	626	22	32.4	630	6	US-10-893-584-274	Sequence 274, App
554	22	32.4	334	7	US-11-127-817-14	Sequence 14, Appli	627	22	32.4	641	7	US-11-094-519A-29	Sequence 29, Appli
555	22	32.4	334	7	US-11-127-877-69	Sequence 69, Appli	628	22	32.4	655	7	US-11-045-802-29	Sequence 29, Appli
556	22	32.4	336	6	US-10-454-437-230	Sequence 230, App	629	22	32.4	664	6	US-10-821-234-1670	Sequence 1670, Ap
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564	22	32.4	377	6	US-10-525-674-22	Sequence 22, Appli	637	22	32.4	725	6	US-10-467-657-1536	Sequence 1536, Ap
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567	22	32.4	387	7	US-11-092-140-17	Sequence 17, Appli	640	22	32.4	730	6	US-10-821-234-1019	Sequence 1019, Ap
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570	22	32.4	393	6	US-10-467-657-1038	Sequence 1038, Ap	643	22	32.4	778	6	US-10-467-657-1686	Sequence 1686, Ap
571	22	32.4	394	6	US-10-131-826A-520	Sequence 520, App	644	22	32.4	783	7	US-11-186-284-59	Sequence 59, Appli
572	22	32.4	395	7	US-11-075-185-13	Sequence 13, Appli	645	22	32.4	784	6	US-10-517-939-324	Sequence 324, App
573	22	32.4	397	6	US-10-641-678-32	Sequence 32, Appli	646	22	32.4	787	6	US-10-517-939-54	Sequence 54, Appli
574	22	32.4	400	6	US-10-467-657-2702	Sequence 2702, Ap	647	22	32.4	795	7	US-11-109-157A-14	Sequence 14, Appli
575	22	32.4	402	6	US-10-793-626-2282	Sequence 2282, Ap	648	22	32.4	801	6	US-10-467-657-6470	Sequence 6470, Ap
576	22	32.4	416	6	US-10-641-678-73	Sequence 73, Appli	649	22	32.4	861	6	US-10-467-657-1286	Sequence 1286, Ap
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583	22	32.4	421	6	US-10-858-730-202	Sequence 202, App	656	22	32.4	898	7	US-11-166-730-3	Sequence 3, Appli
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587	22	32.4	431	6	US-10-793-626-2566	Sequence 2566, Ap	660	22	32.4	1065	7	US-11-191-374-16	Sequence 16, Appli
588	22	32.4	433	7	US-11-047-383-2	Sequence 2, Appli	661	22	32.4	1065	7	US-11-191-375-16	Sequence 16, Appli
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593	22	32.4	447	6	US-10-467-657-7050	Sequence 7050, Ap	666	22	32.4	1069	7	US-11-191-374-17	Sequence 17, Appli
594	22	32.4	456	7	US-11-074-176-238	Sequence 238, App	667	22	32.4	1069	7	US-11-191-375-17	Sequence 17, Appli
595	22	32.4	461	6	US-10-509-464-7	Sequence 7, Appli	668	22	32.4	1069	7	US-11-191-588-17	Sequence 17, Appli
596	22	32.4	461	7	US-11-082-389-176	Sequence 176, App	669	22	32.4	1072	7	US-11-109-157A-13	Sequence 13, Appli
597	22	32.4	467	6	US-10-467-657-5552	Sequence 5552, Ap	670	22	32.4	1103	7	US-11-109-157A-9	Sequence 9, Appli
598	22	32.4	472	7	US-11-165-211-6	Sequence 6, Appli	671	22	32.4	1165	7	US-11-192-219-2	Sequence 2, Appli
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604	22	32.4	475	6	US-10-467-657-5382	Sequence 5382, Ap	677	22	32.4	2084	6	US-10-055-877-252	Sequence 252, App
605	22	32.4	475	6	US-10-467-657-7376	Sequence 7376, Ap	678	22	32.4	2107	6	US-10-055-877-73	Sequence 73, Appli
606	22	32.4	484	7	US-11-052-554A-170	Sequence 170, App	679	22	32.4	2107	6	US-10-995-561-827	Sequence 827, App
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683	22	32.4	2353	7	US-11-097-728-6	Sequence 6, Appli
684	22	32.4	2480	6	US-10-995-561-825	Sequence 825, App
685	22	32.4	2612	6	US-10-453-372-38	Sequence 38, Appl
686	22	32.4	2669	6	US-10-453-372-36	Sequence 36, Appl
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688	22	32.4	3104	6	US-10-453-372-62	Sequence 62, Appl
689	22	32.4	3104	6	US-10-453-372-64	Sequence 64, Appl
690	22	32.4	3116	6	US-10-995-561-826	Sequence 826, App
691	22	32.4	3130	6	US-10-453-372-42	Sequence 42, Appl
692	22	32.4	3194	7	US-11-052-554A-90	Sequence 90, Appl
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695	22	32.4	3567	6	US-10-453-372-1112	Sequence 1112, Ap
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697	22	32.4	4868	7	US-11-044-111-24	Sequence 24, Appl
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699	21.5	31.6	152	7	US-11-034-569-4	Sequence 4, Appli
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707	21.5	31.6	555	7	US-11-034-569-8	Sequence 8, Appli
708	21.5	31.6	560	7	US-11-034-569-6	Sequence 6, Appli
709	21.5	31.6	1798	6	US-10-995-561-1033	Sequence 1033, Ap
710	21.5	31.6	1798	6	US-10-995-561-1034	Sequence 1034, Ap
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714	21	30.9	9	7	US-11-033-039-247	Sequence 247, App
715	21	30.9	11	7	US-11-105-708-9	Sequence 9, Appli
716	21	30.9	11	7	US-11-038-980-14	Sequence 14, Appl
717	21	30.9	12	6	US-10-763-286A-37	Sequence 37, Appl
718	21	30.9	12	7	US-11-116-144-85	Sequence 85, Appl
719	21	30.9	13	7	US-11-038-980-23	Sequence 23, Appl
720	21	30.9	14	6	US-10-467-657-9100	Sequence 9100, Ap
721	21	30.9	14	7	US-11-033-039-261	Sequence 261, App
722	21	30.9	17	6	US-10-939-890-368	Sequence 368, App
723	21	30.9	18	6	US-10-763-286A-38	Sequence 38, Appl
724	21	30.9	19	7	US-11-196-919-7	Sequence 7, Appli
725	21	30.9	21	6	US-10-939-890-369	Sequence 369, App
726	21	30.9	21	6	US-10-939-890-511	Sequence 511, App
727	21	30.9	22	6	US-10-209-208-19	Sequence 19, Appl
728	21	30.9	22	6	US-10-467-657-8846	Sequence 8846, Ap
729	21	30.9	22	7	US-11-218-880-19	Sequence 19, Appl
730	21	30.9	24	6	US-10-989-226-31	Sequence 31, Appl
731	21	30.9	24	7	US-11-066-967-58	Sequence 58, Appl
732	21	30.9	30	7	US-11-156-843-57	Sequence 57, Appl
733	21	30.9	30	7	US-11-156-843-63	Sequence 63, Appl
734	21	30.9	30	7	US-11-156-843-70	Sequence 70, Appl
735	21	30.9	30	7	US-11-156-843-86	Sequence 86, Appl
736	21	30.9	30	7	US-11-156-843-89	Sequence 89, Appl
737	21	30.9	34	6	US-10-467-657-5458	Sequence 5458, Ap
738	21	30.9	34	7	US-11-121-301-82	Sequence 82, Appl
739	21	30.9	35	7	US-11-174-816-82	Sequence 82, Appl
740	21	30.9	35	7	US-11-174-816-83	Sequence 83, Appl
741	21	30.9	35	7	US-11-174-816-84	Sequence 84, Appl
742	21	30.9	35	7	US-11-174-819-101	Sequence 101, App
743	21	30.9	35	7	US-11-174-819-102	Sequence 102, App
744	21	30.9	35	7	US-11-174-819-103	Sequence 103, App
745	21	30.9	38	7	US-11-027-111-22	Sequence 22, Appl
746	21	30.9	39	6	US-10-467-657-3574	Sequence 3574, Ap
747	21	30.9	40	7	US-11-068-783-77	Sequence 77, Appl
748	21	30.9	43	6	US-10-467-657-7886	Sequence 7886, Ap
749	21	30.9	45	6	US-10-467-657-8264	Sequence 8264, Ap
750	21	30.9	46	6	US-10-467-657-7732	Sequence 7732, Ap
751	21	30.9	51	6	US-10-467-657-9096	Sequence 9096, Ap
752	21	30.9	55	6	US-10-467-657-8693	Sequence 8693, Ap
753	21	30.9	58	7	US-11-008-570-104	Sequence 104, App
754	21	30.9	60	7	US-11-091-668-6	Sequence 6, Appli
755	21	30.9	63	6	US-10-914-391A-6	Sequence 6, Appli

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757	21	30.9	63	7	US-11-008-570-100	Sequence 100, App
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761	21	30.9	76	7	US-11-000-463-790	Sequence 790, App
762	21	30.9	78	6	US-10-467-657-1782	Sequence 1782, Ap
763	21	30.9	80	7	US-11-226-325-131	Sequence 131, App
764	21	30.9	80	7	US-11-166-412-113	Sequence 113, App
765	21	30.9	82	7	US-11-055-822-456	Sequence 456, App
766	21	30.9	83	6	US-10-467-657-7926	Sequence 7926, Ap
767	21	30.9	87	6	US-10-839-799-112	Sequence 112, App
768	21	30.9	88	7	US-11-194-890-1	Sequence 1, Appli
769	21	30.9	91	5	US-09-978-360A-801	Sequence 801, App
770	21	30.9	95	7	US-11-198-847-227	Sequence 227, App
771	21	30.9	95	7	US-11-008-570-118	Sequence 118, App
772	21	30.9	96	7	US-11-075-351-60	Sequence 60, Appl
773	21	30.9	96	7	US-10-467-657-4214	Sequence 4214, Ap
774	21	30.9	98	6	US-10-530-253-36	Sequence 36, Appl
775	21	30.9	98	6	US-10-467-657-7214	Sequence 7214, Ap
776	21	30.9	99	6	US-10-467-657-9162	Sequence 9162, Ap
777	21	30.9	100	6	US-10-467-657-9162	Sequence 9162, Ap
778	21	30.9	101	6	US-10-467-657-6454	Sequence 6454, Ap
779	21	30.9	106	7	US-11-008-727-12	Sequence 12, Appl
780	21	30.9	106	7	US-11-073-222-3	Sequence 3, Appli
781	21	30.9	106	7	US-11-052-554A-360	Sequence 360, App
782	21	30.9	114	6	US-10-986-501-190	Sequence 190, App
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785	21	30.9	126	6	US-10-793-626-2272	Sequence 2272, Ap
786	21	30.9	126	6	US-10-467-657-2050	Sequence 2050, Ap
787	21	30.9	126	7	US-11-221-900-11	Sequence 11, Appl
788	21	30.9	127	7	US-11-052-554A-312	Sequence 312, App
789	21	30.9	129	6	US-10-501-039-8	Sequence 8, Appli
790	21	30.9	129	7	US-11-073-222-2	Sequence 2, Appli
791	21	30.9	130	7	US-11-055-822-690	Sequence 690, App
792	21	30.9	130	7	US-11-055-822-768	Sequence 768, App
793	21	30.9	137	7	US-11-022-562-225	Sequence 225, App
794	21	30.9	138	5	US-09-978-360A-483	Sequence 483, App
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796	21	30.9	140	6	US-10-980-388-93	Sequence 93, Appl
797	21	30.9	142	6	US-10-467-657-7870	Sequence 7870, Ap
798	21	30.9	142	6	US-10-856-751-37	Sequence 37, Appl
799	21	30.9	143	6	US-10-467-657-274	Sequence 274, App
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803	21	30.9	156	6	US-10-467-657-3808	Sequence 3808, Ap
804	21	30.9	157	6	US-10-467-657-4360	Sequence 4360, Ap
805	21	30.9	157	6	US-10-467-657-5496	Sequence 5496, Ap
806	21	30.9	159	6	US-10-467-657-5114	Sequence 5114, Ap
807	21	30.9	160	6	US-10-846-172A-10	Sequence 10, Appl
808	21	30.9	162	5	US-09-978-360A-585	Sequence 585, App
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810	21	30.9	164	6	US-10-793-626-2398	Sequence 2398, Ap
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813	21	30.9	167	6	US-10-467-657-5306	Sequence 5306, Ap
814	21	30.9	171	6	US-10-714-887-400	Sequence 400, App
815	21	30.9	174	7	US-11-055-822-838	Sequence 838, App
816	21	30.9	175	6	US-10-467-657-7504	Sequence 7504, Ap
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825	21	30.9	191	6	US-10-467-657-4100	Sequence 4100, Ap
826	21	30.9	191	6	US-10-467-657-7442	Sequence 7442, Ap
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828	21	30.9	191	6	US-10-519-390-6	Sequence 6, Appli

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830	21	30.9	191	6	US-10-714-887-56	Sequence 56, Appl	903	21	30.9	272	7	US-11-000-463-277	Sequence 277, App
831	21	30.9	191	7	US-11-033-365-160	Sequence 160, App	904	21	30.9	274	7	US-11-082-389-150	Sequence 150, App
832	21	30.9	192	7	US-11-033-365-159	Sequence 159, App	905	21	30.9	280	6	US-10-873-528-49	Sequence 49, Appl
833	21	30.9	192	7	US-11-033-365-197	Sequence 197, App	906	21	30.9	281	6	US-10-467-657-1352	Sequence 1352, Ap
834	21	30.9	192	7	US-11-033-365-198	Sequence 198, App	907	21	30.9	282	6	US-10-878-556A-125	Sequence 125, App
835	21	30.9	192	7	US-11-033-365-200	Sequence 200, App	908	21	30.9	283	6	US-10-632-150-50	Sequence 50, Appl
836	21	30.9	192	7	US-11-187-522-1	Sequence 1, Appl1	909	21	30.9	283	7	US-11-073-457-50	Sequence 50, Appl
837	21	30.9	193	6	US-10-467-657-674	Sequence 674, App	910	21	30.9	283	7	US-11-073-460-50	Sequence 50, Appl
838	21	30.9	193	7	US-11-033-365-196	Sequence 196, App	911	21	30.9	284	6	US-10-714-887-128	Sequence 128, App
839	21	30.9	196	7	US-11-033-365-199	Sequence 199, App	912	21	30.9	285	7	US-11-082-389-324	Sequence 324, App
840	21	30.9	198	6	US-10-467-657-5440	Sequence 5440, Ap	913	21	30.9	286	6	US-10-954-468-25	Sequence 25, Appl
841	21	30.9	202	7	US-11-144-889A-2	Sequence 2, Appl1	914	21	30.9	286	7	US-11-055-822-44	Sequence 44, Appl
842	21	30.9	202	7	US-11-166-412-128	Sequence 128, App	915	21	30.9	287	6	US-10-954-468-17	Sequence 17, Appl
843	21	30.9	202	7	US-11-166-412-143	Sequence 143, App	916	21	30.9	287	6	US-10-954-468-24	Sequence 24, Appl
844	21	30.9	208	7	US-11-055-822-462	Sequence 462, App	917	21	30.9	287	7	US-11-080-991-66	Sequence 66, Appl
845	21	30.9	208	7	US-11-055-822-704	Sequence 704, App	918	21	30.9	287	7	US-11-054-281-322	Sequence 322, App
846	21	30.9	208	7	US-11-170-653-52	Sequence 52, Appl	919	21	30.9	288	6	US-10-467-657-82	Sequence 82, Appl
847	21	30.9	209	5	US-09-978-360A-665	Sequence 665, App	920	21	30.9	288	6	US-10-467-657-5918	Sequence 5918, Ap
848	21	30.9	209	7	US-11-055-822-88	Sequence 88, Appl	921	21	30.9	288	6	US-10-954-468-20	Sequence 20, Appl
849	21	30.9	210	7	US-11-055-822-90	Sequence 90, Appl	922	21	30.9	288	6	US-10-954-468-22	Sequence 22, Appl
850	21	30.9	210	5	US-09-978-360A-538	Sequence 538, App	923	21	30.9	288	6	US-10-954-468-23	Sequence 23, Appl
851	21	30.9	211	6	US-10-467-657-6800	Sequence 6800, Ap	924	21	30.9	289	6	US-10-954-468-19	Sequence 19, Appl
852	21	30.9	213	6	US-10-892-379-6	Sequence 6, Appl1	925	21	30.9	289	6	US-10-954-468-21	Sequence 21, Appl
853	21	30.9	214	6	US-10-892-379-5	Sequence 5, Appl1	926	21	30.9	290	6	US-10-131-826A-222	Sequence 222, App
854	21	30.9	215	6	US-10-996-007B-27	Sequence 27, Appl	927	21	30.9	290	6	US-10-954-468-18	Sequence 18, Appl
855	21	30.9	216	6	US-10-883-512-77	Sequence 77, Appl	928	21	30.9	291	6	US-10-467-657-4148	Sequence 4148, Ap
856	21	30.9	217	6	US-10-467-657-388	Sequence 388, App	929	21	30.9	291	6	US-10-467-657-6508	Sequence 6508, Ap
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859	21	30.9	217	6	US-10-467-657-3800	Sequence 3800, Ap	932	21	30.9	294	7	US-11-055-822-480	Sequence 480, App
860	21	30.9	217	6	US-10-467-657-3930	Sequence 3930, Ap	933	21	30.9	294	7	US-11-055-822-880	Sequence 880, App
861	21	30.9	217	6	US-10-467-657-4018	Sequence 4018, Ap	934	21	30.9	295	7	US-11-194-246-298	Sequence 298, App
862	21	30.9	217	6	US-10-467-657-4438	Sequence 4438, Ap	935	21	30.9	298	6	US-10-467-657-4362	Sequence 4362, Ap
863	21	30.9	217	6	US-10-467-657-4802	Sequence 4802, Ap	936	21	30.9	298	6	US-10-454-437-384	Sequence 384, App
864	21	30.9	217	6	US-10-467-657-6518	Sequence 6518, Ap	937	21	30.9	298	7	US-11-179-977-6	Sequence 6, Appl1
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866	21	30.9	218	6	US-10-995-561-830	Sequence 830, App	939	21	30.9	298	7	US-11-055-822-878	Sequence 878, App
867	21	30.9	219	6	US-10-846-172A-1	Sequence 1, Appl1	940	21	30.9	299	6	US-10-467-657-4424	Sequence 4424, Ap
868	21	30.9	222	7	US-11-124-368A-208	Sequence 208, App	941	21	30.9	299	6	US-10-878-556A-94	Sequence 5794, Ap
869	21	30.9	223	6	US-10-467-657-3974	Sequence 3974, Ap	942	21	30.9	302	6	US-10-467-657-5794	Sequence 5794, Ap
870	21	30.9	224	6	US-10-892-379-7	Sequence 7, Appl1	943	21	30.9	303	7	US-11-186-284-193	Sequence 193, App
871	21	30.9	228	6	US-10-467-657-8358	Sequence 8358, Ap	944	21	30.9	303	7	US-11-054-281-82	Sequence 82, Appl
872	21	30.9	232	6	US-10-467-657-4338	Sequence 4338, Ap	945	21	30.9	303	7	US-11-054-281-83	Sequence 83, Appl
873	21	30.9	233	7	US-11-170-653-53	Sequence 53, Appl	946	21	30.9	304	6	US-10-846-172A-5	Sequence 5, Appl1
874	21	30.9	234	6	US-10-793-626-2580	Sequence 2580, Ap	947	21	30.9	305	7	US-11-080-991-92	Sequence 92, Appl
875	21	30.9	236	7	US-11-140-965-4	Sequence 4, Appl1	948	21	30.9	306	6	US-10-467-657-4304	Sequence 4304, Ap
876	21	30.9	238	7	US-11-008-727-26	Sequence 26, Appl	949	21	30.9	306	7	US-11-102-497-13	Sequence 13, Appl
877	21	30.9	239	7	US-11-000-463-875	Sequence 875, App	950	21	30.9	308	6	US-10-467-657-3236	Sequence 3236, Ap
878	21	30.9	239	7	US-11-000-463-876	Sequence 876, App	951	21	30.9	309	6	US-10-524-647-110	Sequence 110, App
879	21	30.9	242	7	US-11-150-883-12	Sequence 12, Appl	952	21	30.9	309	6	US-10-714-887-62	Sequence 62, Appl
880	21	30.9	243	6	US-10-131-826A-164	Sequence 164, App	953	21	30.9	310	6	US-10-714-887-52	Sequence 52, Appl
881	21	30.9	244	6	US-10-793-626-134	Sequence 134, App	954	21	30.9	310	7	US-11-082-389-306	Sequence 306, App
882	21	30.9	245	6	US-10-793-626-1042	Sequence 1042, Ap	955	21	30.9	310	7	US-11-055-163-7	Sequence 7, Appl1
883	21	30.9	250	7	US-11-054-515-933	Sequence 933, App	956	21	30.9	311	7	US-11-055-822-246	Sequence 246, App
884	21	30.9	253	7	US-11-080-991-42	Sequence 42, Appl	957	21	30.9	311	7	US-11-156-084-202	Sequence 202, App
885	21	30.9	254	6	US-10-467-657-5138	Sequence 5138, Ap	958	21	30.9	312	7	US-11-008-570-41	Sequence 41, Appl
886	21	30.9	254	7	US-11-067-323-1033	Sequence 1033, Ap	959	21	30.9	312	7	US-11-008-570-42	Sequence 42, Appl
887	21	30.9	254	7	US-11-067-323-1081	Sequence 1081, Ap	960	21	30.9	313	7	US-11-052-554A-316	Sequence 316, App
888	21	30.9	255	6	US-10-846-172A-4	Sequence 4, Appl1	961	21	30.9	313	7	US-11-152-569-13	Sequence 13, Appl
889	21	30.9	257	6	US-10-793-626-3244	Sequence 3244, Ap	962	21	30.9	313	7	US-11-024-959-356	Sequence 356, App
890	21	30.9	258	7	US-11-054-515-1365	Sequence 1365, Ap	963	21	30.9	313	7	US-11-054-281-18	Sequence 18, Appl
891	21	30.9	259	6	US-10-467-657-3410	Sequence 3410, Ap	964	21	30.9	313	7	US-11-054-281-81	Sequence 81, Appl
892	21	30.9	259	6	US-10-763-712A-116	Sequence 116, App	965	21	30.9	314	7	US-11-183-914-3	Sequence 3, Appl1
893	21	30.9	261	6	US-10-467-657-4282	Sequence 4282, Ap	966	21	30.9	314	7	US-11-008-570-43	Sequence 43, Appl
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896	21	30.9	266	6	US-10-982-545-3	Sequence 3, Appl1	969	21	30.9	317	7	US-11-094-519A-38	Sequence 38, Appl
897	21	30.9	266	6	US-10-821-234-1334	Sequence 1334, Ap	970	21	30.9	318	6	US-10-632-150-42	Sequence 42, Appl
898	21	30.9	267	6	US-10-846-172A-2	Sequence 2, Appl1	971	21	30.9	318	7	US-11-073-457-42	Sequence 42, Appl
899	21	30.9	269	7	US-11-000-463-403	Sequence 403, App	972	21	30.9	318	7	US-11-000-463-331	Sequence 331, App
900	21	30.9	270	7	US-11-008-727-24	Sequence 24, Appl	973	21	30.9	318	7	US-11-000-463-803	Sequence 803, App
901	21	30.9	271	7	US-11-179-977-10	Sequence 10, Appl	974	21	30.9	318	7	US-11-073-460-42	Sequence 42, Appl

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977	21	30.9	322	6	US-10-524-647-18	Sequence 18, Appl
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979	21	30.9	323	6	US-10-525-674-8	Sequence 8, Appli
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981	21	30.9	324	6	US-10-467-657-722	Sequence 722, App
982	21	30.9	326	7	US-11-024-959-446	Sequence 446, App
983	21	30.9	326	7	US-11-024-959-447	Sequence 447, App
984	21	30.9	327	6	US-10-467-962B-107	Sequence 107, App
985	21	30.9	328	6	US-10-995-561-884	Sequence 884, App
986	21	30.9	330	6	US-10-846-172A-7	Sequence 7, Appli
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989	21	30.9	332	6	US-10-454-437-42	Sequence 42, Appl
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991	21	30.9	335	6	US-10-995-561-866	Sequence 866, App
992	21	30.9	336	6	US-10-478-345-4	Sequence 4, Appli
993	21	30.9	336	6	US-10-793-626-3210	Sequence 3210, Ap
994	21	30.9	336	7	US-11-152-892-4	Sequence 4, Appli
995	21	30.9	339	6	US-10-821-234-1098	Sequence 1098, Ap
996	21	30.9	340	6	US-10-067-974-8	Sequence 8, Appli
997	21	30.9	340	7	US-11-055-822-42	Sequence 42, Appl
998	21	30.9	340	7	US-11-055-822-452	Sequence 452, App
999	21	30.9	342	7	US-11-152-892-11	Sequence 11, Appl
1000	21	30.9	343	7	US-11-009-658-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-11-112-277-16
; Sequence 16, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to AEEA-MPA
US-11-112-277-16

Query Match 80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 7 CFGGRMDRIGAQSGLGC 23

RESULT 2

US-11-112-277-50
; Sequence 50, Application US/11112277
; Publication No. US20050267293A1

; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to MPA
US-11-112-277-50

Query Match 80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 7 CFGGRMDRIGAQSGLGC 23

RESULT 3

US-11-112-277-51
; Sequence 51, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to EEEEP-MPA
US-11-112-277-51

Query Match 80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 7 CFGGRMDRIGAQSGLGC 23

RESULT 4

US-11-059-814-4
; Sequence 4, Application US/11059814
; Publication No. US20050272650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
; TITLE OF INVENTION: Proliferation Disorders
; FILE REFERENCE: USF-215PTCZ
; CURRENT APPLICATION NUMBER: US/11/059,814
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-814-4

Query Match 80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 7 CFGGRMDRIGAQSGLGC 23

RESULT 5

US-11-175-690-309
; Sequence 309, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haselcline et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 309
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-309

Query Match 80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 7 CFGGRMDRIGAQSGLGC 23

RESULT 6
US-10-510-880-3
; Sequence 3, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righspospitalet
; TITLE OF INVENTION: Methods for determining levels of human
; TITLE OF INVENTION: B-type natriuretic peptide precursors
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-510-880-3

Query Match 80.9%; Score 55; DB 6; Length 121;
Best Local Similarity 58.8%; Pred. No. 5.9e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 99 CFGHKIDRIGSVSRLGC 115

RESULT 7

US-10-977-334-5
; Sequence 5, Application US/10977334
; Publication No. US20050244904A1
; GENERAL INFORMATION:
; APPLICANT: NG, LEONG
; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
; FILE REFERENCE: ISA-016.01
; CURRENT APPLICATION NUMBER: US/10/977,334
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/542,647
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: GB 0325279.8
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-334-5

Query Match 80.9%; Score 55; DB 6; Length 126;
Best Local Similarity 58.8%; Pred. No. 6.1e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
Db 110 CFGKLIDRIGSMSGLGC 126

RESULT 8

US-10-510-880-2
; Sequence 2, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righspospitalet


```
; TITLE OF INVENTION: Methods for determining levels of human
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-510-880-2
```

```
Query Match      80.9%; Score 55; DB 6; Length 131;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 CFGXXXDRIGXXSXGC 17
      ||| |||| | ||
Db      109 CFGRRLDRIQSLGSLGC 125
```

RESULT 9

```
US-11-059-814-7
; Sequence 7, Application US/11059814
; Publication No. US20050272650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
; FILE REFERENCE: USF-215PTCZ
; CURRENT APPLICATION NUMBER: US/11/059,814
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-814-7
```

```
Query Match      80.9%; Score 55; DB 7; Length 151;
Best Local Similarity 58.8%; Pred. No. 7.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 CFGXXXDRIGXXSXGC 17
      ||| |||| | ||
Db      130 CFGGRMDRIGAQSLGCL 146
```

RESULT 10

```
US-11-059-814-16
; Sequence 16, Application US/11059814
; Publication No. US20050272650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
; FILE REFERENCE: USF-215PTCZ
; CURRENT APPLICATION NUMBER: US/11/059,814
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 16
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-059-814-16
```

```
Query Match      80.9%; Score 55; DB 7; Length 152;
Best Local Similarity 58.8%; Pred. No. 7.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 CFGXXXDRIGXXSXGC 17
      ||| |||| | ||
Db      129 CFGGRIDRIGAQSLGCL 145
```

RESULT 11

```
US-10-977-334-4
; Sequence 4, Application US/10977334
; Publication No. US20050244904A1
; GENERAL INFORMATION:
; APPLICANT: NG, LEONG
; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
; FILE REFERENCE: ISA-016.01
; CURRENT APPLICATION NUMBER: US/10/977,334
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/542,647
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: GB 0325279.8
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-334-4
```

```
Query Match      80.9%; Score 55; DB 6; Length 153;
Best Local Similarity 58.8%; Pred. No. 7.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 CFGXXXDRIGXXSXGC 17
      ||| |||| | ||
Db      130 CFGGRMDRIGAQSLGCL 146
```

RESULT 12

```
US-11-175-690-222
; Sequence 222, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-222

```

```

Query Match      80.9%; Score 55; DB 7; Length 637;
Best Local Similarity 58.8%; Pred. No. 0.00027;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      31 CFGGRMDRIGAGSGLGC 47

```

RESULT 13

```

US-11-175-690-321
; Sequence 321, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 321
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-321

```

```

Query Match      73.5%; Score 50; DB 7; Length 26;
Best Local Similarity 52.9%; Pred. No. 0.00016;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      10 CFGGRKMDRISSSSGLGC 26

```

RESULT 14

```

US-11-175-690-322
; Sequence 322, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22

```

```

; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 322
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-322

```

```

Query Match      73.5%; Score 50; DB 7; Length 27;
Best Local Similarity 52.9%; Pred. No. 0.00016;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      10 CFGGRKMDRISSSSGLGC 26

```

RESULT 15

```

US-11-175-690-371
; Sequence 371, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 371
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-371

```

```

Query Match      73.5%; Score 50; DB 7; Length 27;
Best Local Similarity 52.9%; Pred. No. 0.00016;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      10 CFGGRKMDRISSSSGLGC 26

```

RESULT 16

```
US-11-175-690-323
; Sequence 323, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 323
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-323
```

```
Query Match      73.5%; Score 50; DB 7; Length 28;
Best Local Similarity 52.9%; Pred. No. 0.00017;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFEXXXXRIGXXSXXGC 17
          |||  |||  |||  |||
Db      10 CFGRKMDRISSSSGLGC 26
```

```
RESULT 17
US-11-175-690-369
; Sequence 369, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 369
; LENGTH: 28
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-11-175-690-369
```

```
Query Match      73.5%; Score 50; DB 7; Length 28;
Best Local Similarity 52.9%; Pred. No. 0.00017;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFEXXXXRIGXXSXXGC 17
          |||  |||  |||  |||
Db      10 CFGRKMDRISSSSGLGC 26
```

```
RESULT 18
US-11-175-690-314
; Sequence 314, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 314
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-314
```

```
Query Match      73.5%; Score 50; DB 7; Length 29;
Best Local Similarity 52.9%; Pred. No. 0.00018;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFEXXXXRIGXXSXXGC 17
          |||  |||  |||  |||
Db      10 CFGRKMDRISSSSGLGC 26
```

```
RESULT 19
US-11-175-690-315
; Sequence 315, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
```

```
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 315
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-315
```

```
Query Match      73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXGXC 17
      ||| ||| | ||
Db      10 CFGRKMDRISSSSGLGC 26
```

RESULT 20

```
US-10-510-880-4
; Sequence 4, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righesopitalec
; TITLE OF INVENTION: Methods for determining levels of human
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-880-4
```

```
Query Match      73.5%; Score 50; DB 6; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXGXC 17
      ||| ||| | ||
Db      10 CFGRKMDRISSSSGLGC 26
```

RESULT 21

```
US-10-977-334-3
; Sequence 3, Application US/10977334
; Publication No. US20050244904A1
; GENERAL INFORMATION:
; APPLICANT: NG, LEONG
; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
; FILE REFERENCE: ISA-016.01
; CURRENT APPLICATION NUMBER: US/10/977,334
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/542,647
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: GB 0325279.8
; PRIOR FILING DATE: 2003-10-29
```

```
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-334-3
```

```
Query Match      73.5%; Score 50; DB 6; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXGXC 17
      ||| ||| | ||
Db      10 CFGRKMDRISSSSGLGC 26
```

RESULT 22

```
US-11-043-590-17
; Sequence 17, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use the
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-17
```

```
Query Match      73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXGXC 17
      ||| ||| | ||
Db      10 CFGRKMDRISSSSGLGC 26
```

RESULT 23

```
US-11-175-690-288
; Sequence 288, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 288
; LENGTH: 32
```



```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-288

Query Match          73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
        ||| ||| | ||
Db       10 CFGRKMDRISSSSGLGC 26

RESULT 24
US-11-175-690-298
; Sequence 298, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 298
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-298

Query Match          73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
        ||| ||| | ||
Db       10 CFGRKMDRISSSSGLGC 26

RESULT 25
US-11-175-690-304
; Sequence 304, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
```

```
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 304
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-304

Query Match          73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
        ||| ||| | ||
Db       10 CFGRKMDRISSSSGLGC 26

RESULT 26
US-11-175-690-317
; Sequence 317, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 317
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-317

Query Match          73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
        ||| ||| | ||
Db       10 CFGRKMDRISSSSGLGC 26

RESULT 27
US-11-175-690-318
; Sequence 318, Application US/11175690
; Publication No. US20060014254A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-318

Query Match      73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXGC 17
Db      10 CFGRKMDRISSSSGLGC 26

RESULT 28
US-11-175-690-370
; Sequence 370, Application US/11/175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 370
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-370
```

```
Query Match      73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXGC 17
Db      10 CFGRKMDRISSSSGLGC 26

RESULT 29
US-11-043-590-15
; Sequence 15, Application US/11/043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use therefor
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 15
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-15

Query Match      73.5%; Score 50; DB 7; Length 42;
Best Local Similarity 52.9%; Pred. No. 0.00025;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXGC 17
Db      20 CFGRKMDRISSSSGLGC 36

RESULT 30
US-11-175-690-368
; Sequence 368, Application US/11/175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 368
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-368

Query Match      73.5%; Score 50; DB 7; Length 52;
Best Local Similarity 52.9%; Pred. No. 0.0003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

OY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 31

US-11-043-590-16
; Sequence 16, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 16
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-16

Query Match 73.5%; Score 50; DB 7; Length 60;
Best Local Similarity 52.9%; Pred. No. 0.00034;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 32

US-10-510-880-5
; Sequence 5, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righospitalet
; TITLE OF INVENTION: Methods for determining levels of human
; TITLE OF INVENTION: B-type natriuretic peptide precursors
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-880-5

Query Match 73.5%; Score 50; DB 6; Length 108;
Best Local Similarity 52.9%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 86 CFGRKMDRISSSSGLGC 102

RESULT 33

US-10-875-800-1
; Sequence 1, Application US/10875800
; Publication No. US20050255484A1
; GENERAL INFORMATION:
; APPLICANT: VALKIRS, GUNARS
; APPLICANT: DAHLEN, JEFF
; APPLICANT: KIRCHICK, HOWARD

; APPLICANT: BUECHLER, KEN
; TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 071949-5408
; CURRENT APPLICATION NUMBER: US/10/875,800
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/10/714,078
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 10/371,149
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/225,082
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT/US02/26604
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/313,775
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/334,964
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/346,485
; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-875-800-1

Query Match 73.5%; Score 50; DB 6; Length 108;
Best Local Similarity 52.9%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 86 CFGRKMDRISSSSGLGC 102

RESULT 34

US-10-299-977-1
; Sequence 1, Application US/10299977
; Publication No. US20050287613A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; APPLICANT: Kupchak, Peter
; APPLICANT: Stanton, Eric
; APPLICANT: Davey, Michelle
; TITLE OF INVENTION: Polyclonal-Polyclonal ELISA Assay For Detecting N-Terminus ProBNP
; FILE REFERENCE: 2132.127
; CURRENT APPLICATION NUMBER: US/10/299,977
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-977-1

Query Match 73.5%; Score 50; DB 6; Length 108;
Best Local Similarity 52.9%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 86 CFGRKMDRISSSSGLGC 102

RESULT 35

US-10-510-880-1
; Sequence 1, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.

```
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righesopspitalet
; TITLE OF INVENTION: Methods for determining levels of human
; TITLE OF INVENTION: B-type natriuretic peptide precursors
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-510-880-1
```

```
Query Match      73.5%; Score 50; DB 6; Length 134;
Best Local Similarity 52.9%; Pred. No. 0.00072;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      112 CFGRKMDRISSSSGLGC 128
```

```
RESULT 36
US-10-875-800-2
```

```
; Sequence 2, Application US/10875800
; Publication No. US20050255484A1
; GENERAL INFORMATION:
; APPLICANT: VALKIRS, GUNARS
; APPLICANT: DAHLEN, JEFF
; APPLICANT: KIRCHICK, HOWARD
; APPLICANT: BUECHLER, KEN
; TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 071949-5408
; CURRENT APPLICATION NUMBER: US/10/875,800
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/10/714,078
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 10/371,149
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/225,082
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT/US02/26604
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/313,775
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/334,964
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/346,485
; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-875-800-2
```

```
Query Match      73.5%; Score 50; DB 6; Length 134;
Best Local Similarity 52.9%; Pred. No. 0.00072;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      112 CFGRKMDRISSSSGLGC 128
```

```
RESULT 37
US-11-043-590-12
; Sequence 12, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use the
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-043-590-12
```

```
Query Match      73.5%; Score 50; DB 7; Length 134;
Best Local Similarity 52.9%; Pred. No. 0.00072;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      112 CFGRKMDRISSSSGLGC 128
```

```
RESULT 38
US-11-043-590-13
```

```
; Sequence 13, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use the
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-043-590-13
```

```
Query Match      73.5%; Score 50; DB 7; Length 162;
Best Local Similarity 52.9%; Pred. No. 0.00086;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      112 CFGRKMDRISSSSGLGC 128
```

```
RESULT 39
US-11-175-690-234
```

```
; Sequence 234, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haselaine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
```



```

; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-234

```

```

Query Match      73.5%; Score 50; DB 7; Length 630;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      29 CFGRKMDRISSSSGLGC 45

```

```

RESULT 40
US-11-175-690-235
; Sequence 235, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 235
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-235

```

```

Query Match      73.5%; Score 50; DB 7; Length 631;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      29 CFGRKMDRISSSSGLGC 45

```

```

RESULT 41
US-11-175-690-236
; Sequence 236, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605

```

```

; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 236
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-236

```

```

Query Match      73.5%; Score 50; DB 7; Length 632;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      29 CFGRKMDRISSSSGLGC 45

```

```

RESULT 42
US-11-175-690-228
; Sequence 228, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 228
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-228

```

```

Query Match      73.5%; Score 50; DB 7; Length 633;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

QY 1 CFGXXXDRIGXXSXXGC 17
 ||| ||| ||| |||
 DB 29 CFGRKMDRISSSSGLGC 45

RESULT 43
 US-11-175-690-211

; Sequence 211, Application US/11175690
 ; Publication No. US20060014254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haseltine et al.
 ; TITLE OF INVENTION: Albumin Fusion Proteins
 ; FILE REFERENCE: PF605
 ; CURRENT APPLICATION NUMBER: US/11/175,690
 ; CURRENT FILING DATE: 2005-07-07
 ; PRIOR APPLICATION NUMBER: PCT/US04/001369
 ; PRIOR FILING DATE: 2004-01-20
 ; PRIOR APPLICATION NUMBER: US 60/441,305
 ; PRIOR FILING DATE: 2003-01-22
 ; PRIOR APPLICATION NUMBER: US 60/453,201
 ; PRIOR FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: US 60/467,222
 ; PRIOR FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: US 60/472,816
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: US 60/476,267
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: US 60/505,172
 ; PRIOR FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US 60/506,746
 ; NUMBER OF SEQ ID NOS: 568
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 211
 ; LENGTH: 641
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-175-690-211

Query Match 73.5%; Score 50; DB 7; Length 641;
 Best Local Similarity 52.9%; Pred. No. 0.003;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
 ||| ||| ||| |||
 DB 34 CFGRKMDRISSSSGLGC 50

RESULT 44
 US-11-175-690-230

; Sequence 230, Application US/11175690
 ; Publication No. US20060014254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haseltine et al.
 ; TITLE OF INVENTION: Albumin Fusion Proteins
 ; FILE REFERENCE: PF605
 ; CURRENT APPLICATION NUMBER: US/11/175,690
 ; CURRENT FILING DATE: 2005-07-07
 ; PRIOR APPLICATION NUMBER: PCT/US04/001369
 ; PRIOR FILING DATE: 2004-01-20
 ; PRIOR APPLICATION NUMBER: US 60/441,305
 ; PRIOR FILING DATE: 2003-01-22
 ; PRIOR APPLICATION NUMBER: US 60/453,201
 ; PRIOR FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: US 60/467,222
 ; PRIOR FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: US 60/472,816
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: US 60/476,267
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: US 60/505,172
 ; PRIOR FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US 60/506,746

; PRIOR FILING DATE: 2003-09-30
 ; NUMBER OF SEQ ID NOS: 568
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 230
 ; LENGTH: 641
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-175-690-230

Query Match 73.5%; Score 50; DB 7; Length 641;
 Best Local Similarity 52.9%; Pred. No. 0.003;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
 ||| ||| ||| |||
 DB 34 CFGRKMDRISSSSGLGC 50

RESULT 45
 US-11-175-690-281

; Sequence 281, Application US/11175690
 ; Publication No. US20060014254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haseltine et al.
 ; TITLE OF INVENTION: Albumin Fusion Proteins
 ; FILE REFERENCE: PF605
 ; CURRENT APPLICATION NUMBER: US/11/175,690
 ; CURRENT FILING DATE: 2005-07-07
 ; PRIOR APPLICATION NUMBER: PCT/US04/001369
 ; PRIOR FILING DATE: 2004-01-20
 ; PRIOR APPLICATION NUMBER: US 60/441,305
 ; PRIOR FILING DATE: 2003-01-22
 ; PRIOR APPLICATION NUMBER: US 60/453,201
 ; PRIOR FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: US 60/467,222
 ; PRIOR FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: US 60/472,816
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: US 60/476,267
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: US 60/505,172
 ; PRIOR FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US 60/506,746
 ; NUMBER OF SEQ ID NOS: 568
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 281
 ; LENGTH: 661
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-175-690-281

Query Match 73.5%; Score 50; DB 7; Length 661;
 Best Local Similarity 52.9%; Pred. No. 0.0031;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
 ||| ||| ||| |||
 DB 34 CFGRKMDRISSSSGLGC 50

RESULT 46
 US-11-175-690-284

; Sequence 284, Application US/11175690
 ; Publication No. US20060014254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haseltine et al.
 ; TITLE OF INVENTION: Albumin Fusion Proteins
 ; FILE REFERENCE: PF605
 ; CURRENT APPLICATION NUMBER: US/11/175,690
 ; CURRENT FILING DATE: 2005-07-07
 ; PRIOR APPLICATION NUMBER: PCT/US04/001369
 ; PRIOR FILING DATE: 2004-01-20

```
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-175-690-284
```

```
Query Match          73.5%; Score 50; DB 7; Length 663;
Best Local Similarity 52.9%; Pred. No. 0.0031;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXXGC 17
Db      34 CFGRKMDRISSSSGLGC 50
```

RESULT 47

```
US-11-175-690-282
; Sequence 282, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 282
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-175-690-282
```

```
Query Match          73.5%; Score 50; DB 7; Length 665;
Best Local Similarity 52.9%; Pred. No. 0.0031;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXXGC 17
Db      34 CFGRKMDRISSSSGLGC 50
```

RESULT 48

```
US-11-175-690-227
; Sequence 227, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-175-690-227
```

```
Query Match          73.5%; Score 50; DB 7; Length 667;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      1 CFGXXXDRIGXXSXXGC 17
Db      34 CFGRKMDRISSSSGLGC 50
```

RESULT 49

```
US-11-175-690-283
; Sequence 283, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 283
```

; LENGTH: 670
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-283

Query Match 73.5%; Score 50; DB 7; Length 670;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXSGC 17
Db 31 CFGRKMDRISSSSGLGC 47

RESULT 50
US-11-175-690-201

; Sequence 201, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haselcine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 201
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-201

Query Match 73.5%; Score 50; DB 7; Length 673;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXSGC 17
Db 34 CFGRKMDRISSSSGLGC 50

Search completed: January 26, 2006, 14:47:30
Job time : 9 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 14:38:26 ; Search time 77 Seconds
(without alignments)
97.006 Million cell updates/sec

Title: US-10-664-605-5
Perfect score: 68
Sequence: 1 CFGXXDXDRIGXXSXGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	82.4	17	5	ABG98259 Human C-t
2	56	82.4	17	5	ABG98264 Human C-t
3	56	82.4	17	5	ABG98241 Human C-t
4	56	82.4	17	5	ABG98246 Human C-t
5	56	82.4	17	5	ABG98269 Human C-t
6	56	82.4	17	5	ABG98211 Human C-t
7	56	82.4	18	2	AAR40630 Human C-t
8	56	82.4	18	2	AAR40624 Human C-t
9	56	82.4	18	2	AAR40627 Human C-t
10	56	82.4	18	2	AAR40621 Human C-t
11	56	82.4	20	2	AAR40455 Human C-t
12	56	82.4	20	2	AAR40449 Human C-t
13	56	82.4	20	2	AAR40434 Human C-t
14	56	82.4	20	2	AAR40454 Human C-t
15	56	82.4	20	2	AAR40428 Human C-t
16	56	82.4	20	4	AAB91293 Human C-t
17	56	82.4	20	5	ABB05585 Human C-t
18	56	82.4	21	2	AAR03304 Human C-t
19	56	82.4	21	2	AAR40629 Human C-t
20	56	82.4	21	2	AAR40620 Human C-t
21	56	82.4	21	2	AAR40623 Human C-t
22	56	82.4	21	2	AAR40626 Human C-t
23	56	82.4	21	4	AAB91294 Human C-t
24	56	82.4	23	2	AAR40448 Human C-t

25	56	82.4	23	2	AAR36975 ANVP #39.
26	56	82.4	23	2	AAR36964 ANVP #28.
27	56	82.4	23	2	AAR40427 [D-Ala132
28	56	82.4	23	2	AAR40622 [Arg129] f
29	56	82.4	23	2	AAR40625 [Arg128] f
30	56	82.4	23	2	AAR40628 [Arg129] f
31	56	82.4	23	2	AAR40619 [Arg129] f
32	56	82.4	24	2	AAR03303 FANP-24 f
33	56	82.4	24	2	AAR04818 Peptide w
34	56	82.4	24	2	AAR04813 Peptide a
35	56	82.4	24	2	AAR40453 [D-Ala143
36	56	82.4	24	2	AAR40446 [D-Ala142
37	56	82.4	24	2	AAR40432 [D-Ala133
38	56	82.4	24	2	AAR40452 [D-Ala143
39	56	82.4	24	2	AAR40431 [D-Ala133
40	56	82.4	24	2	AAR40425 [D-Ala132
41	56	82.4	24	2	AAR40426 [D-Ala132
42	56	82.4	24	2	AAR40447 [D-Ala142
43	56	82.4	24	2	AAW70091 Atrial na
44	56	82.4	24	4	AAB91295 Atrial-na
45	56	82.4	24	4	AAB91292 Atrial-na
46	56	82.4	24	4	AAE12435 Frog atri
47	56	82.4	24	9	ADV86892 Bovine AN
48	56	82.4	25	2	AAR40424 [D-Ala132
49	56	82.4	25	2	AAR40587 [Ala132] r
50	56	82.4	25	2	AAR40451 [D-Ala143
51	56	82.4	25	2	AAR36943 ANVP #7.
52	56	82.4	25	2	AAR40445 [D-Ala142
53	56	82.4	25	2	AAR40423 [D-Ala132
54	56	82.4	25	2	AAR40450 [D-Ala143
55	56	82.4	25	2	AAR36954 ANVP #18.
56	56	82.4	25	2	AAR40588 [Ala133] h
57	56	82.4	25	2	AAR40429 [D-Ala133
58	56	82.4	25	2	AAR40444 [D-Val142
59	56	82.4	25	2	AAR40430 [D-Ala133
60	56	82.4	28	2	AAR93687 hANP(1-28
61	56	82.4	28	2	AAW93099 Natriturec
62	56	82.4	28	6	ADA00824 Human hAN
63	56	82.4	28	6	ADA00776 Human hAN
64	56	82.4	30	4	AAB91296 Atrial-na
65	55	80.9	17	1	AAp61004 Atrial na
66	55	80.9	17	1	AAp71036 Peptide w
67	55	80.9	17	1	AAp71034 Peptide w
68	55	80.9	17	1	AAp82493 Cyclic pe
69	55	80.9	17	2	AAR25952 CNP analo
70	55	80.9	17	4	AAB91298 Atrial-na
71	55	80.9	17	5	ABG98247 Human C-t
72	55	80.9	17	5	ABG98248 Human C-t
73	55	80.9	17	5	ABG98263 Human C-t
74	55	80.9	17	5	ABG98260 Human C-t
75	55	80.9	17	5	ABG98244 Human C-t
76	55	80.9	17	5	ABG98268 Human C-t
77	55	80.9	17	5	ABG98242 Human C-t
78	55	80.9	17	5	ABG98265 Human C-t
79	55	80.9	17	5	ABG98203 Human C-t
80	55	80.9	17	5	ABG98257 Human C-t
81	55	80.9	17	5	ABG98243 Human C-t
82	55	80.9	17	5	ABG98262 Human C-t
83	55	80.9	17	5	ABG98267 Human C-t
84	55	80.9	17	5	ABG98245 Human C-t
85	55	80.9	17	5	ABG98261 Human C-t
86	55	80.9	17	5	ABG98270 Human C-t
87	55	80.9	17	5	ABG98255 Human C-t
88	55	80.9	17	6	AAE37841 Rat C-cyp
89	55	80.9	17	6	AAE37839 Rat atria
90	55	80.9	17	6	AAE37840 Rat brain
91	55	80.9	18	2	AAR36963 ANVP #27.
92	55	80.9	18	2	AAR40601 [Arg128] r
93	55	80.9	18	2	AAR40600 [Arg128] r
94	55	80.9	18	2	AAR40642 [Arg129] f
95	55	80.9	18	2	AAR40639 [Arg128] f
96	55	80.9	18	2	AAR40604 [Arg129] h
97	55	80.9	18	2	AAR40650 [D-Arg128

98	55	80.9	18	2	AAR40653	Aar40653 [D-Arg129	171	55	80.9	22	2	AAR36959	Aar36959 ANVP #23.
99	55	80.9	18	2	AAR40605	Aar40605 [Arg129]h	172	55	80.9	22	2	AAW21992	Aaw21992 Porcine C
100	55	80.9	18	2	AAR40611	Aar40611 [Arg129]l	173	55	80.9	22	2	AAW70089	Aaw70089 Alpha hum
101	55	80.9	18	2	AAR40595	Aar40595 [Arg129]h	174	55	80.9	22	3	AAE124081	Aab224081 Human PRO
102	55	80.9	19	1	AAP80902	Aap80902 Human car	175	55	80.9	22	3	AAE124087	Aab10487 Human CNP
103	55	80.9	20	2	AAR04085	Aar04085 Sequence	176	55	80.9	22	4	AAE124087	Aab82551 Human C-t
104	55	80.9	20	2	AAR40474	Aar40474 [D-Cys145	177	55	80.9	22	4	AAE124087	Aab91332 Brain nat
105	55	80.9	20	2	AAR40397	Aar40397 hANVP (127	178	55	80.9	22	4	AAE124087	Aab91342 C-type na
106	55	80.9	20	2	AAR40403	Aar40403 [D-Cys129	179	55	80.9	22	4	AAE124087	Aab91341 C-type na
107	55	80.9	20	2	AAR40506	Aar40506 [D-Arg127	180	55	80.9	22	4	AAE124087	Aab91299 Atxial-na
108	55	80.9	20	2	AAR36942	Aar36942 ANVP #6.	181	55	80.9	22	4	AAE124087	Aab45741 Human C-t
109	55	80.9	20	2	AAR40500	Aar40500 [D-Arg126	182	55	80.9	22	4	AAE124087	Aae12440 Chicken C
110	55	80.9	20	2	AAR40574	Aar40574 [Phe134]r	183	55	80.9	22	4	AAE12433	Aae12433 Frog atri
111	55	80.9	20	2	AAR40689	Aar40689 [Nle133]r	184	55	80.9	22	4	AAE12433	Aae12439 C-type na
112	55	80.9	20	2	AAR40409	Aar40409 [D-Cys130	185	55	80.9	22	4	AAE12441	Aae12441 Frog C-cy
113	55	80.9	20	2	AAR40393	Aar40393 rANVP (126	186	55	80.9	22	4	AAE12441	Aab70811 Human nat
114	55	80.9	20	2	AAR40694	Aar40694 [Nle134]h	187	55	80.9	22	5	ABG98202	Abg98202 Human C-t
115	55	80.9	20	2	AAR40392	Aar40392 rANVP (126	188	55	80.9	22	6	ADA00766	Ada00766 Human nat
116	55	80.9	20	2	AAR40396	Aar40396 hANVP (127	189	55	80.9	22	6	ABU63217	Abu63217 N-termnu
117	55	80.9	20	2	AAR40480	Aar40480 [D-Cys146	190	55	80.9	22	6	ABU63218	Abu63218 Human C-t
118	55	80.9	21	1	AAP60769	Aap60769 Rat atrio	191	55	80.9	22	8	ADL122343	Adl122343 Natrlurec
119	55	80.9	21	1	AAP71371	Aap71371 Antihyper	192	55	80.9	22	8	ADL122343	Adl122343 Natrlurec
120	55	80.9	21	2	AAR36962	Aar36962 ANVP #26.	193	55	80.9	22	8	ADL122353	Adl122353 Natrlurec
121	55	80.9	21	2	AAR40603	Aar40603 [Arg129]h	194	55	80.9	22	8	ADL122347	Adl122347 Natrlurec
122	55	80.9	21	2	AAR40607	Aar40607 [Arg128]l	195	55	80.9	22	8	ADL122344	Adl122344 Natrlurec
123	55	80.9	21	2	AAR40594	Aar40594 [Arg128]r	196	55	80.9	22	8	ADL122344	Adl122344 Natrlurec
124	55	80.9	21	2	AAR40638	Aar40638 [D-Arg128	197	55	80.9	22	9	ADL122344	Adl122344 Natrlurec
125	55	80.9	21	2	AAR40638	Aar40638 [Arg128]l	198	55	80.9	22	9	ADL122344	Adl122344 Natrlurec
126	55	80.9	21	2	AAR40641	Aar40641 [Arg129]l	199	55	80.9	22	9	ADL122344	Adl122344 Natrlurec
127	55	80.9	21	2	AAR40647	Aar40647 [Arg129]l	200	55	80.9	22	9	ADL122344	Adl122344 Natrlurec
128	55	80.9	21	2	AAR40610	Aar40610 [Arg129]l	201	55	80.9	23	1	ADL122344	Adl122344 Natrlurec
129	55	80.9	21	2	AAR40652	Aar40652 [D-Arg129	202	55	80.9	23	1	ADL122344	Adl122344 Natrlurec
130	55	80.9	21	4	AAB91307	Aab91307 Atxial-na	203	55	80.9	23	1	ADL122344	Adl122344 Natrlurec
131	55	80.9	22	1	AAP50904	Aap50904 Sequence	204	55	80.9	23	1	ADL122344	Adl122344 Natrlurec
132	55	80.9	22	1	AAP71374	Aap71374 Antihyper	205	55	80.9	23	1	ADL122344	Adl122344 Natrlurec
133	55	80.9	22	1	AAP83168	Aap83168 Atxial Na	206	55	80.9	23	1	ADL122344	Adl122344 Natrlurec
134	55	80.9	22	1	AAP83177	Aap83177 Atxial Na	207	55	80.9	23	1	ADL122344	Adl122344 Natrlurec
135	55	80.9	22	1	AAP82832	Aap82832 Human Atr	208	55	80.9	23	1	ADL122344	Adl122344 Natrlurec
136	55	80.9	22	2	AAR14792	Aar14792 C-type na	209	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
137	55	80.9	22	2	AAR25712	Aar25712 Atxial na	210	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
138	55	80.9	22	2	AAR29774	Aar29774 Atxial na	211	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
139	55	80.9	22	2	AAR25705	Aar25705 Atxial na	212	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
140	55	80.9	22	2	AAR29773	Aar29773 Atxial na	213	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
141	55	80.9	22	2	AAR25415	Aar25415 Atxial na	214	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
142	55	80.9	22	2	AAR29721	Aar29721 Brain pep	215	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
143	55	80.9	22	2	AAR29722	Aar29722 CNP analo	216	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
144	55	80.9	22	2	AAR29730	Aar29730 CNP analo	217	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
145	55	80.9	22	2	AAR29730	Aar29730 CNP analo	218	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
146	55	80.9	22	2	AAR29731	Aar29731 CNP analo	219	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
147	55	80.9	22	2	AAR29731	Aar29731 CNP analo	220	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
148	55	80.9	22	2	AAR29916	Aar29916 CNP analo	221	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
149	55	80.9	22	2	AAR25954	Aar25954 CNP analo	222	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
150	55	80.9	22	2	AAR25955	Aar25955 CNP analo	223	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
151	55	80.9	22	2	AAR25956	Aar25956 CNP analo	224	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
152	55	80.9	22	2	AAR29726	Aar29726 CNP analo	225	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
153	55	80.9	22	2	AAR29915	Aar29915 CNP analo	226	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
154	55	80.9	22	2	AAR29723	Aar29723 CNP analo	227	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
155	55	80.9	22	2	AAR29729	Aar29729 CNP analo	228	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
156	55	80.9	22	2	AAR29918	Aar29918 CNP analo	229	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
157	55	80.9	22	2	AAR29720	Aar29720 CNP analo	230	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
158	55	80.9	22	2	AAR29724	Aar29724 CNP analo	231	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
159	55	80.9	22	2	AAR29917	Aar29917 CNP analo	232	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
160	55	80.9	22	2	AAR25953	Aar25953 CNP analo	233	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
161	55	80.9	22	2	AAR21589	Aar21589 ANF (7-28	234	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
162	55	80.9	22	2	AAR21588	Aar21588 ANF (7-28	235	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
163	55	80.9	22	2	AAR32254	Aar32254 Human CNP	236	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
164	55	80.9	22	2	AAR40602	Aar40602 [Arg129]h	237	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
165	55	80.9	22	2	AAR40644	Aar40644 [Arg128]l	238	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
166	55	80.9	22	2	AAR40646	Aar40646 [Arg129]l	239	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
167	55	80.9	22	2	AAR40597	Aar40597 [Arg129]h	240	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
168	55	80.9	22	2	AAR40592	Aar40592 [Arg128]r	241	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
169	55	80.9	22	2	AAR36961	Aar36961 ANVP #25.	242	55	80.9	23	2	ADL122344	Adl122344 Natrlurec
170	55	80.9	22	2	AAR40598	Aar40598 [Arg129]h	243	55	80.9	23	2	ADL122344	Adl122344 Natrlurec

244	55	80.9	23	2	AAR40637	Aar40637 [Arg128] I	317	55	80.9	25	2	AAR40443	Aar40443 [D-Ser141
245	55	80.9	23	2	AAR40643	Aar40643 [Arg128] I	318	55	80.9	25	2	AAR40488	Aar40488 [D-Ser148
246	55	80.9	23	2	AAR40695	Aar40695 [Nle134]h	319	55	80.9	25	2	AAR40508	Aar40508 [D-Ser128
247	55	80.9	23	2	AAR36973	Aar36973 ANVP #37.	320	55	80.9	25	2	AAR36937	Aar36937 ANVP #1.
248	55	80.9	23	2	AAR40593	Aar40593 [Arg139]r	321	55	80.9	25	2	AAR40404	Aar40404 [D-Cys130
249	55	80.9	23	2	AAR40612	Aar40612 [Arg128] I	322	55	80.9	25	2	AAR40441	Aar40441 [D-Ala139
250	55	80.9	23	4	AAB91308	Aab91308 Atrial-na	323	55	80.9	25	2	AAR40475	Aar40475 [D-Cys146
251	55	80.9	23	4	AAB91348	Aab91348 C-type na	324	55	80.9	25	2	AAR40482	Aar40482 [D-Asn147
252	55	80.9	23	4	AAB91305	Aab91305 Atrial-na	325	55	80.9	25	2	AAR40388	Aar40388 hANVP (127
253	55	80.9	24	1	AAP50848	Aap50848 Sequence	326	55	80.9	25	2	AAR40405	Aar40405 [D-Cys130
254	55	80.9	24	1	AAP51230	Aap51230 Sequence	327	55	80.9	25	2	AAR40410	Aar40410 [D-Phe130
255	55	80.9	24	1	AAP60771	Aap60771 Rat atrio	328	55	80.9	25	2	AAR40484	Aar40484 [D-Asn147
256	55	80.9	24	1	AAP70964	Aap70964 Sequence	329	55	80.9	25	2	AAR40489	Aar40489 [D-Asn148
257	55	80.9	24	1	AAP94848	Aap94848 Sequence	330	55	80.9	25	2	AAR40494	Aar40494 [D-Phe149
258	55	80.9	24	1	AAP94850	Aap94850 Sequence	331	55	80.9	25	2	AAR40507	Aar40507 [D-Ser127
259	55	80.9	24	2	AAR04102	Aar04102 Intranasal	332	55	80.9	25	2	AAR40746	Aar40746 [D-Asp136
260	55	80.9	24	2	AAR36940	Aar36940 ANVP #4.	333	55	80.9	25	2	AAR36939	Aar36939 ANVP #3.
261	55	80.9	24	2	AAR40389	Aar40389 hANVP (127	334	55	80.9	25	2	AAR36944	Aar36944 ANVP #8.
262	55	80.9	24	2	AAR40485	Aar40485 [D-Asn147	335	55	80.9	25	2	AAR36945	Aar36945 ANVP #9.
263	55	80.9	24	2	AAR40490	Aar40490 [D-Ser148	336	55	80.9	25	2	AAR36953	Aar36953 ANVP #17.
264	55	80.9	24	2	AAR40390	Aar40390 hANVP (127	337	55	80.9	25	2	AAR40745	Aar40745 [D-Asp135
265	55	80.9	24	2	AAR40401	Aar40401 [D-Cys129	338	55	80.9	25	2	AAR40398	Aar40398 [D-Cys129
266	55	80.9	24	2	AAR40686	Aar40686 [Nle133]r	339	55	80.9	25	2	AAR36955	Aar36955 ANVP #19.
267	55	80.9	24	2	AAR40692	Aar40692 [Nle134]h	340	55	80.9	25	2	AAR40399	Aar40399 [D-Cys129
268	55	80.9	24	2	AAR40478	Aar40478 [D-Cys146	341	55	80.9	25	2	AAR40743	Aar40743 [D-Ile137
269	55	80.9	24	2	AAR40503	Aar40503 [D-Arg127	342	55	80.9	25	2	AAR36946	Aar36946 ANVP #10.
270	55	80.9	24	2	AAR40400	Aar40400 [D-Cys129	343	55	80.9	25	2	AAR40691	Aar40691 [Nle134]h
271	55	80.9	24	2	AAR40486	Aar40486 [D-Asn147	344	55	80.9	25	2	AAR40470	Aar40470 [D-Cys145
272	55	80.9	24	2	AAR40472	Aar40472 [D-Cys145	345	55	80.9	25	2	AAR40493	Aar40493 [D-Phe148
273	55	80.9	24	2	AAR40693	Aar40693 [Nle134]h	346	55	80.9	25	2	AAR40495	Aar40495 [D-Arg126
274	55	80.9	24	2	AAR40406	Aar40406 [D-Cys130	347	55	80.9	25	2	AAR40711	Aar40711 [Lys134]h
275	55	80.9	24	2	AAR36938	Aar36938 ANVP #2.	348	55	80.9	25	2	AAR40744	Aar40744 [D-Ile138
276	55	80.9	24	2	AAR40391	Aar40391 rANVP (126	349	55	80.9	25	2	AAR36948	Aar36948 ANVP #12.
277	55	80.9	24	2	AAR40477	Aar40477 [D-Cys146	350	55	80.9	25	2	AAR40481	Aar40481 [D-Asn146
278	55	80.9	24	2	AAR40471	Aar40471 [D-Cys145	351	55	80.9	25	2	AAR40483	Aar40483 [D-Asn147
279	55	80.9	24	2	AAR40687	Aar40687 [Nle133]r	352	55	80.9	25	2	AAR40496	Aar40496 [D-Arg126
280	55	80.9	24	2	AAR40407	Aar40407 [D-Cys130	353	55	80.9	25	2	AAR40690	Aar40690 [Nle134]h
281	55	80.9	24	2	AAR40491	Aar40491 [D-Ser148	354	55	80.9	25	2	AAR40748	Aar40748 [D-Ala140
282	55	80.9	24	2	AAR40498	Aar40498 [D-Arg126	355	55	80.9	25	2	AAR40476	Aar40476 [D-Cys146
283	55	80.9	24	2	AAR40504	Aar40504 [D-Arg127	356	55	80.9	25	2	AAR40502	Aar40502 [D-Arg127
284	55	80.9	24	2	AAR40571	Aar40571 [Phe134]r	357	55	80.9	25	2	AAR42952	Aar42952 Polypepti
285	55	80.9	24	2	AAR40572	Aar40572 [Phe134]r	358	55	80.9	25	4	AAB91312	Aab91312 Atrial-na
286	55	80.9	24	2	AAR40497	Aar40497 [D-Arg126	359	55	80.9	25	4	AAB91304	Aab91304 Atrial-na
287	55	80.9	24	4	AAB91297	Aab91297 Atrial-na	360	55	80.9	25	8	ADL73465	Adl73465 Atrial na
288	55	80.9	24	4	AAB91311	Aab91311 Atrial-na	361	55	80.9	26	1	AAP50113	Aap50113 Biologica
289	55	80.9	24	4	AAB91329	Aab91329 Atrial-na	362	55	80.9	26	1	AAP51106	Aap51106 Sequence
290	55	80.9	24	4	AAB91326	Aab91326 Atrial-na	363	55	80.9	26	1	AAP60807	Aap60807 Atrial na
291	55	80.9	24	4	AAB91309	Aab91309 Atrial-na	364	55	80.9	26	1	AAP71129	Aap71129 Sequence
292	55	80.9	24	4	ADL22345	Adl22345 Natriuret	365	55	80.9	26	1	AAP70966	Aap70966 Sequence
293	55	80.9	24	8	ADL22346	Adl22346 Natriuret	366	55	80.9	26	1	AAR04816	Aar04816 Peptide w
294	55	80.9	24	8	ADL22346	Adl22346 Natriuret	367	55	80.9	26	2	AAR08309	Aar08309 Chelated
295	55	80.9	25	1	AAP51233	Aap51233 Sequence	368	55	80.9	26	2	AAR04812	Aar04812 Peptide a
296	55	80.9	25	1	AAP51236	Aap51236 Sequence	369	55	80.9	26	2	AAR21586	Aar21586 ANF (3-28
297	55	80.9	25	1	AAP51229	Aap51229 Sequence	370	55	80.9	26	2	AAB91302	Aab91302 Atrial-na
298	55	80.9	25	1	AAP51232	Aap51232 Sequence	371	55	80.9	26	4	AAB91335	Aab91335 Brain nat
299	55	80.9	25	1	AAP61016	Aap61016 Alpha-fra	372	55	80.9	26	4	AAB91303	Aab91303 Atrial-na
300	55	80.9	25	1	AAP61025	Aap61025 Peptide h	373	55	80.9	26	4	AAP71464	Aap71464 Sequence
301	55	80.9	25	1	AAP71467	Aap71467 Sequence	374	55	80.9	27	1	AAP60084	Aap60084 Sequence
302	55	80.9	25	2	AAR40456	Aar40456 [D-Ileu143	375	55	80.9	27	1	AAP70970	Aap70970 Sequence
303	55	80.9	25	2	AAR40510	Aar40510 [D-Ser129	376	55	80.9	27	1	AAR11853	Aar11853 Bel natri
304	55	80.9	25	2	AAR40685	Aar40685 [Nle133]r	377	55	80.9	27	2	AAR25950	Aar25950 CNP analo
305	55	80.9	25	2	AAR36952	Aar36952 ANVP #16.	378	55	80.9	27	2	AAR62357	Aar62357 Vasonatri
306	55	80.9	25	2	AAR36956	Aar36956 ANVP #20.	379	55	80.9	27	2	AAR62358	Aar62358 Vasonatri
307	55	80.9	25	2	AAR40501	Aar40501 [D-Arg127	380	55	80.9	27	4	AAB91306	Aab91306 Atrial-na
308	55	80.9	25	2	AAR40569	Aar40569 [Phe134]r	381	55	80.9	27	4	AAB91315	Aab91315 Atrial-na
309	55	80.9	25	2	AAR40570	Aar40570 [Lys133]r	382	55	80.9	27	4	AAB91325	Aab91325 Atrial-na
310	55	80.9	25	2	AAR40684	Aar40684 [Nle133]r	383	55	80.9	27	4	ADL92008	Adl92008 Vasonatri
311	55	80.9	25	2	AAR40742	Aar40742 [D-Ile134	384	55	80.9	27	8	ADN03415	Adn03415 Exemplary
312	55	80.9	25	2	AAR36950	Aar36950 ANVP #14.	385	55	80.9	27	8	Vasonatri	
313	55	80.9	25	2	AAR36951	Aar36951 ANVP #15.	386	55	80.9	27	8	Vasonatri	
314	55	80.9	25	2	AAR40387	Aar40387 rANVP (126	387	55	80.9	27	8	Vasonatri	
315	55	80.9	25	2			388	55	80.9	27	8		
316	55	80.9	25	2			389	55	80.9	27	8		

390	55	80.9	28	1	AAP50048	Aap50048	Cardionat
391	55	80.9	28	1	AAP50172	Aap50172	Sequence
392	55	80.9	28	1	AAP50118	Aap50118	Sequence
393	55	80.9	28	1	AAP60076	Aap60076	Sequence
394	55	80.9	28	1	AAP61015	Aap61015	Alpha-fra
395	55	80.9	28	1	AAP61400	Aap61400	Alpha-hum
396	55	80.9	28	1	AAP71696	Aap71696	Actrial na
397	55	80.9	28	1	AAP71202	Aap71202	Lysine fr
398	55	80.9	28	1	AAP70655	Aap70655	Sequence
399	55	80.9	28	1	AAP71419	Aap71419	7, 23-Cys (
400	55	80.9	28	1	AAP82005	Aap82005	Diuretic
401	55	80.9	28	1	AAP91314	Aap91314	Sequence
402	55	80.9	28	2	AAR03305	Aar03305	Rat atria
403	55	80.9	28	2	AAR03306	Aar03306	Human atr
404	55	80.9	28	2	AAR04819	Aar04819	Peptide w
405	55	80.9	28	2	AAR04815	Aar04815	Peptide w
406	55	80.9	28	2	AAR05859	Aar05859	Actrial na
407	55	80.9	28	2	AAR04941	Aar04941	Actrial na
408	55	80.9	28	2	AAR03415	Aar03415	N-termi
409	55	80.9	28	2	AAR04811	Aar04811	Peptide a
410	55	80.9	28	2	AAR03302	Aar03302	Sequence
411	55	80.9	28	2	AAR29725	Aar29725	CNP analo
412	55	80.9	28	2	AAR40042	Aar40042	Leu- (Gly)
413	55	80.9	28	2	AAR37109	Aar37109	Protected
414	55	80.9	28	2	AAR37110	Aar37110	human atr
415	55	80.9	28	2	AAR87093	Aar87093	Actrial na
416	55	80.9	28	2	AAW11624	Aaw11624	Target pe
417	55	80.9	28	2	AAW70088	Aaw70088	Alpha rat
418	55	80.9	28	2	AAW70087	Aaw70087	Alpha hum
419	55	80.9	28	2	AAW51308	Aaw51308	Human A-t
420	55	80.9	28	2	AAW62656	Aaw62656	Human atr
421	55	80.9	28	2	AAW93094	Aaw93094	Natriuret
422	55	80.9	28	3	AAW80216	Aay80216	Human A-t
423	55	80.9	28	3	AAW98488	Aay98488	Pep 23 us
424	55	80.9	28	3	AAO20102	Aao20102	Sequence
425	55	80.9	28	3	AAO20103	Aao20103	Alpha-hum
426	55	80.9	28	4	AAW82549	Aab82549	Human atr
427	55	80.9	28	4	AAW45841	Aab45841	Nucleic a
428	55	80.9	28	4	AAW81020	Aab81020	Actrial na
429	55	80.9	28	4	AAW91319	Aab91319	Actrial-na
430	55	80.9	28	4	AAW91310	Aab91310	Actrial-na
431	55	80.9	28	4	AAW45740	Aab45740	Human A-t
432	55	80.9	28	4	AAU04278	Aau04278	Nuclear 1
433	55	80.9	28	4	AAE12432	Aae12432	Rat atria
434	55	80.9	28	4	AAE12431	Aae12431	Human atr
435	55	80.9	28	4	AAW70809	Aab70809	Human nat
436	55	80.9	28	4	AAW85983	Aau85983	Modified
437	55	80.9	28	5	AAW80710	Aag80710	Human ANP
438	55	80.9	28	5	ABW98204	Abg98204	Human atr
439	55	80.9	28	6	ADA00783	Ada00783	Human nat
440	55	80.9	28	6	ADA00825	Ada00825	Human hAN
441	55	80.9	28	6	ADA00771	Ada00771	Rat natr
442	55	80.9	28	6	ADA00822	Ada00822	Human hAN
443	55	80.9	28	6	ADA00823	Ada00823	Human hAN
444	55	80.9	28	6	ADA00785	Ada00785	Rat natr
445	55	80.9	28	6	ABW63214	Abu63214	Human atr
446	55	80.9	28	7	ADW17067	Adf17067	Human alb
447	55	80.9	28	8	ADW92004	Adl92004	Actrial na
448	55	80.9	28	8	ADW22342	Adl22342	Natriuret
449	55	80.9	28	8	ADW22349	Adl22349	Natriuret
450	55	80.9	28	8	ADW22337	Adl22337	Natriuret
451	55	80.9	28	8	ADW22334	Adl22334	Natriuret
452	55	80.9	28	8	ADW22331	Adl22331	Natriuret
453	55	80.9	28	8	ADW22333	Adl22333	Natriuret
454	55	80.9	28	8	ADW22350	Adl22350	Natriuret
455	55	80.9	28	8	ADW22332	Adl22332	Natriuret
456	55	80.9	28	8	ADW41340	Adm41340	Human atr
457	55	80.9	28	8	ADW03290	Adn03290	Exemplary
458	55	80.9	28	8	ADW18406	Adp18406	Neurogene
459	55	80.9	28	8	ADW18427	Adp18427	Neurogene
460	55	80.9	28	8	ADW49288	Adp49288	Natriuret
461	55	80.9	28	8	ADW26469	Adq26469	Post-tran
462	55	80.9	28	8	ADW26469	Adq26469	Post-tran
463	55	80.9	28	8	ADW92528	Adt92528	Cyclic pe
464	55	80.9	28	8	ADW86889	Adv86889	Rat alpha
465	55	80.9	28	9	ADW86888	Adv86888	Human alp
466	55	80.9	28	9	ADW08063	Adw08063	Human bra
467	55	80.9	28	9	ADW95864	Adw95864	Human atr
468	55	80.9	28	9	ADW45305	Adw45305	Human fus
469	55	80.9	28	9	ADW62992	Ady62992	Human atr
470	55	80.9	28	9	ADW4817	Ady4817	Peptide w
471	55	80.9	29	2	AAW04814	Aaw04814	Peptide a
472	55	80.9	29	2	AAW13079	Aaw13079	Tetradeca
473	55	80.9	29	2	AAW13080	Aaw13080	Tetradeca
474	55	80.9	29	2	AAW70094	Aaw70094	Natriuret
475	55	80.9	29	2	AAW67041	Aaw67041	Actrial na
476	55	80.9	29	2	AAW91289	Aab91289	Actrial-na
477	55	80.9	29	4	AAE12438	Aae12438	Chicken b
478	55	80.9	29	4	ADW86895	Adv86895	NP peptid
479	55	80.9	29	8	ADW86895	Adv86895	NP peptid
480	55	80.9	29	9	ADW86895	Adv86895	NP peptid
481	55	80.9	31	1	AAW51105	Aap51105	Sequence
482	55	80.9	31	1	AAW51105	Aap51105	Sequence
483	55	80.9	31	2	AAW31170	Aay31170	Human PSA
484	55	80.9	31	4	AAW71941	Aab71941	Ubiquitin
485	55	80.9	32	1	AAW51104	Aap51104	Sequence
486	55	80.9	32	1	AAW71466	Aap71466	Sequence
487	55	80.9	32	1	AAW71463	Aap71463	Sequence
488	55	80.9	32	1	AAW80388	Aap80388	Sequence
489	55	80.9	32	1	AAW80388	Aap80388	Sequence
490	55	80.9	32	2	AAW70092	Aaw70092	Brain nat
491	55	80.9	32	2	AAW67039	Aaw67039	Actrial na
492	55	80.9	32	2	AAW51301	Aaw51301	Canine B-
493	55	80.9	32	2	AAW51302	Aaw51302	Canine B-
494	55	80.9	32	3	AAW80221	Aay80221	Canine B-
495	55	80.9	32	3	AAW80222	Aay80222	Porcine B
496	55	80.9	32	4	AAW91314	Aab91314	Actrial-na
497	55	80.9	32	4	AAW91331	Aab91331	Actrial-na
498	55	80.9	32	4	AAW91328	Aab91328	Actrial-na
499	55	80.9	32	4	AAW91336	Aab91336	Brain nat
500	55	80.9	32	4	AAW45736	Aab45736	Canine BN
501	55	80.9	32	4	AAE12436	Aae12436	Pig brain
502	55	80.9	32	4	AAW70812	Aab70812	Humanuro
503	55	80.9	32	6	ADA00764	Ada00764	Human nat
504	55	80.9	32	7	ADW17063	Adf17063	Human alb
505	55	80.9	32	8	ADW22340	Adl22340	Natriuret
506	55	80.9	32	8	ADW22339	Adl22339	Natriuret
507	55	80.9	32	8	ADW49281	Adp49281	Natriuret
508	55	80.9	32	8	ADW49276	Adp49276	Natriuret
509	55	80.9	32	8	ADW49301	Adp49301	Natriuret
510	55	80.9	32	8	ADW49301	Adp49301	Natriuret
511	55	80.9	32	9	ADW49301	Adp49301	Natriuret
512	55	80.9	32	9	ADW49301	Adp49301	Natriuret
513	55	80.9	33	1	AAW51103	Aap51103	Sequence
514	55	80.9	35	1	AAW50112	Aap50112	Biologica
515	55	80.9	35	1	AAW60806	Aap60806	Actrial na
516	55	80.9	35	1	AAW61765	Aap61765	Sequence
517	55	80.9	35	1	AAW60270	Aap60270	Sequence
518	55	80.9	35	2	AAW08327	Aar08327	Chelated
519	55	80.9	35	2	AAW08328	Aar08328	Chelated
520	55	80.9	35	2	AAW06352	Aar06352	Actrial na
521	55	80.9	35	2	AAW06353	Aar06353	Actrial na
522	55	80.9	37	2	AAW25986	Aar25986	Ventriculu
523	55	80.9	37	2	AAW65450	Aaw65450	Lebetin d
524	55	80.9	37	2	AAW65450	Aaw65450	Lebetin d
525	55	80.9	37	4	ABW63211	Abu63211	Human C-t
526	55	80.9	37	6	ADW62989	Ady62989	Natriuret
527	55	80.9	38	2	AAW65449	Aaw65449	Lebetin d
528	55	80.9	40	2	AAW21945	Aaw21945	Fusion pr
529	55	80.9	40	2	AAW33021	Aaw33021	Fusion pr
530	55	80.9	42	2	AAW13323	Aar13323	Alpha-hum
531	55	80.9	43	1	AAW60078	Aap60078	Sequence
532	55	80.9	43	1	AAW81211	Aap81211	Alpha-hum
533	55	80.9	45	2	AAW70093	Aaw70093	Brain nat
534	55	80.9	45	2	AAW51304	Aaw51304	Mouse B-t
535	55	80.9	45	2	AAW51303	Aaw51303	Rat B-tyr

536	55	80.9	45	3	AAY80224	Aay80224	Mouse B-t	609	55	80.9	131	7	ADD93294	Add93294	Pig prepr
537	55	80.9	45	3	AAY80223	Aay80223	Rat B-typ	610	55	80.9	131	8	ADM41432	Adm41432	Pig brain
538	55	80.9	45	4	AAB91334	Aab91334	Brain nat	611	55	80.9	133	1	AAP60080	Aap60080	Sequence
539	55	80.9	45	4	AAB91338	Aab91338	Brain nat	612	55	80.9	136	2	AAR36935	Aar36935	Gamma pre
540	55	80.9	45	4	AAE12437	Aae12437	Rat brain	613	55	80.9	140	2	AAR05669	Aar05669	Gamma-chi
541	55	80.9	45	9	ADV86894	Adv86894	Rat BNP p	614	55	80.9	140	6	ADA09507	Ada09507	Canine br
542	55	80.9	46	2	AAW65444	Aaw65444	Lebetin d	615	55	80.9	140	8	ADM41417	Adm41417	Canine br
543	55	80.9	48	1	AAP50115	Aap50115	Rat atria	616	55	80.9	144	2	AAR21677	Aar21677	Beta-gal
544	55	80.9	53	2	AAW16490	Aaw16490	Human C-t	617	55	80.9	144	2	AAR21676	Aar21676	Beta-gal
545	55	80.9	53	2	AAW21991	Aaw21991	Porcine C	618	55	80.9	147	2	AAR03301	Aar03301	Sequence
546	55	80.9	53	2	AD124859	Adi24859	C-type na	619	55	80.9	150	1	AAP51239	Aap51239	Sequence
547	55	80.9	53	4	AAB91344	Aab91344	C-type na	620	55	80.9	150	1	AAP51241	Aap51241	Sequence
548	55	80.9	53	4	AAB91343	Aab91343	C-type na	621	55	80.9	151	1	AAP50050	Aap50050	Cardiodi1
549	55	80.9	53	8	ADL92007	Adl92007	C-type na	622	55	80.9	151	1	AAP50036	Aap50036	Sequence
550	55	80.9	56	4	AAB91313	Aab91313	Attrial-na	623	55	80.9	151	1	AAP70629	Aap70629	Sequence
551	55	80.9	62	1	AAP60165	Aap60165	Rat recom	624	55	80.9	151	2	AAR36934	Aar36934	Human pre
552	55	80.9	71	1	AAP51107	Aap51107	Sequence	625	55	80.9	151	2	AAW98193	Aaw98193	Human atr
553	55	80.9	73	1	AAP51102	Aap51102	Sequence	626	55	80.9	151	8	ADM41415	Adm41415	Human atr
554	55	80.9	88	1	AAP50493	Aap50493	Cardiodi1	627	55	80.9	151	8	ADM41343	Adm41343	Human pre
555	55	80.9	101	9	AEB50531	Aeb50531	Human hea	628	55	80.9	151	8	ADR75285	Adr75285	Human atr
556	55	80.9	103	3	AAB10489	Aab10489	Human pro	629	55	80.9	151	8	ADU05014	Adu05014	Amino aci
557	55	80.9	103	9	ADM46288	Adw46288	Sheep N-t	630	55	80.9	151	8	ADU04663	Adu04663	Human atr
558	55	80.9	103	9	ADM46287	Adw46287	Bovine N-t	631	55	80.9	151	8	ADY34280	Ady34280	Human atr
559	55	80.9	103	9	ADM46291	Adw46291	Rat N-ter	632	55	80.9	151	9	AEB50582	Aeb50582	Human atr
560	55	80.9	103	9	ADM46290	Adw46290	Mouse N-t	633	55	80.9	152	1	AAP51242	Aap51242	Human atr
561	55	80.9	103	9	ADM46292	Adw46292	Pig N-ter	634	55	80.9	152	1	AAP60325	Aap60325	Ggamma-ra
562	55	80.9	103	9	ADM46289	Adw46289	Human N-t	635	55	80.9	152	2	AAR36936	Aar36936	Rat pre-p
563	55	80.9	111	1	AAP50565	Aap50565	Sequence	636	55	80.9	152	2	AAW98191	Aaw98191	Rat atria
564	55	80.9	115	2	AAR29911	Aar29911	Type C na	637	55	80.9	152	8	ADF86020	Adf86020	Truncated
565	55	80.9	116	1	AAP50102	Aap50102	Attrial na	638	55	80.9	152	8	ADM41429	Adm41429	Bovine at
566	55	80.9	118	9	AEB50532	Aeb50532	Human hea	639	55	80.9	152	8	ADM41352	Adm41352	Murine pr
567	55	80.9	120	2	AAR54670	Aar54670	Mouse bra	640	55	80.9	153	7	ADF44952	Adf44952	Human atr
568	55	80.9	120	2	AAR54669	Aar54669	Mouse bra	641	55	80.9	157	8	ADF86021	Adf86021	Truncated
569	55	80.9	121	2	AAR10973	Aar10973	Rat Brain	642	55	80.9	161	5	ABP33228	Abp33228	Human ORF
570	55	80.9	121	2	AAR54668	Aar54668	Mouse bra	643	55	80.9	168	4	AAAB81019	Aab81019	Interleuk
571	55	80.9	121	2	AAR54667	Aar54667	Mouse bra	644	55	80.9	169	9	ADW08082	Adw08082	Dog brain
572	55	80.9	121	7	ADD93295	Add93295	Mouse pre	645	55	80.9	196	7	ADF44937	Adf44937	Heloderma
573	55	80.9	121	8	ADM41431	Adm41431	Rat brain	646	55	80.9	198	5	ABP69270	Abp69270	Human pol
574	55	80.9	121	8	ADM41430	Adm41430	Mouse bra	647	55	80.9	240	2	AAR05425	Aar05425	Amino aci
575	55	80.9	122	2	AAR62682	Aar62682	Hamster b	648	55	80.9	241	1	AAP92070	Aap92070	Bothrops
576	55	80.9	125	1	AAP82656	Aap82656	Vasodilat	649	55	80.9	265	6	ABP56118	Abp56118	Sequence
577	55	80.9	126	1	AAP50037	Aap50037	Sequence	650	55	80.9	340	3	AAO20104	Aao20104	Gene-9 al
578	55	80.9	126	1	AAP51240	Aap51240	Sequence	651	55	80.9	637	9	ADM45218	Adm45218	Human ser
579	55	80.9	126	1	AAP60017	Aap60017	Sequence	652	54	79.4	17	5	ABG98206	Abg98206	Human deg
580	55	80.9	126	2	AAR00582	Aar00582	Human gam	653	54	79.4	17	5	ABG98256	Abg98256	Human C-t
581	55	80.9	126	2	AAR29912	Aar29912	Human CNP	654	54	79.4	17	5	ABG98253	Abg98253	Human C-t
582	55	80.9	126	2	AAR29913	Aar29913	Human CNP	655	54	79.4	17	5	ABG98258	Abg98258	Human C-t
583	55	80.9	126	2	AAR20182	Aar20182	Sequence	656	54	79.4	17	5	ABG98266	Abg98266	Human C-t
584	55	80.9	126	2	AAR22188	Aar22188	Sequence	657	54	79.4	20	2	AAR40580	Aar40580	[Pro132]r
585	55	80.9	126	2	AAR22361	Aar22361	hCNP. 7/1	658	54	79.4	22	2	AAR40586	Aar40586	[Pro133]h
586	55	80.9	126	2	AAR20074	Aar20074	Sequence	659	54	79.4	22	2	AAR25711	Aar25711	Attrial na
587	55	80.9	126	2	AAW16491	Aaw16491	Human C-t	660	54	79.4	22	2	AAR21828	Aar21828	Sequence
588	55	80.9	126	2	AAW21990	Aaw21990	Porcine C	661	54	79.4	23	2	AAR40585	Aar40585	[Pro133]h
589	55	80.9	126	2	AAW34533	Aaw34533	Human atr	662	54	79.4	23	2	AAR36978	Aar36978	ANVP #42.
590	55	80.9	126	3	AAB10488	Aab10488	Human pre	663	54	79.4	23	2	AAR40579	Aar40579	[Pro132]r
591	55	80.9	126	8	ABO84726	Ab084726	Human can	664	54	79.4	24	2	AAR40584	Aar40584	[Pro133]h
592	55	80.9	126	8	ABO84725	Ab084725	Mouse can	665	54	79.4	24	2	AAR40578	Aar40578	[Pro132]r
593	55	80.9	126	8	ADR75286	Adr75286	Human C-t	666	54	79.4	24	2	AAR40577	Aar40577	[Pro132]r
594	55	80.9	126	8	ADR75284	Adr75284	Human atr	667	54	79.4	24	2	AAR40583	Aar40583	[Pro133]h
595	55	80.9	126	8	ADU05015	Adu05015	Amino aci	668	54	79.4	25	1	AAP51234	Aap51234	Sequence
596	55	80.9	126	8	ADU05013	Adu05013	Amino aci	669	54	79.4	25	2	AAR40582	Aar40582	[Pro133]h
597	55	80.9	126	8	ADU04662	Adu04662	Human atr	670	54	79.4	25	2	AAR40576	Aar40576	[Pro132]r
598	55	80.9	126	8	ADU04664	Adu04664	Human C-t	671	54	79.4	25	2	AAR40581	Aar40581	[Pro135]h
599	55	80.9	126	9	ADW95863	Adw95863	Human pro	672	54	79.4	25	2	AAR40575	Aar40575	[Pro132]r
600	55	80.9	126	9	ADY34279	Ady34279	Human atr	673	54	79.4	25	2	AAR40439	Aar40439	[D-Val137
601	55	80.9	126	9	ADY34281	Ady34281	Human C-t	674	54	79.4	25	2	AAR36957	Aar36957	ANVP #21.
602	55	80.9	128	1	AAP51238	Aap51238	Sequence	675	54	79.4	25	2	AAR21587	Aar21587	Polypepti
603	55	80.9	128	8	ADP99246	Adp99246	Attrial na	676	54	79.4	26	2	ADL22336	Adl22336	Natrlurec
604	55	80.9	129	3	AAB23976	Aab23976	Plasmid p	677	54	79.4	28	8	ADL22336	Adl22336	Natrlurec
605	55	80.9	131	2	AAR07342	Aar07342	Porcine B	678	53	77.9	17	5	ABG98252	Abg98252	Human C-t
606	55	80.9	131	2	AAR04084	Aar04084	Oligopept	679	52	76.5	17	5	ABG98250	Abg98250	Human C-t
607	55	80.9	131	2	AAR04086	Aar04086	Protein e	680	52	76.5	22	2	AAR25708	Aar25708	Attrial na
608	55	80.9	131	2	AAR13325	Aar13325	Cla prote	681	52	76.5	24	1	AAP94851	Aap94851	Sequence

682	52	76.5	25	2	AAR40713	Aar40713 [Ly8137]h	755	50	73.5	24	8	ADL22366	Adl22366 Natriuret
683	52	76.5	25	2	AAR40712	Aar40712 [Ly8136]r	756	50	73.5	24	8	ADL22360	Adl22360 Natriuret
684	51	75.0	17	1	AAP71037	Aap71037 Peptide w	757	50	73.5	24	8	ADL22363	Adl22363 Natriuret
685	51	75.0	17	5	ABG98236	Abg98236 Human C-t	758	50	73.5	24	8	ADP49306	Adp49306 Natriuret
686	51	75.0	17	5	ABG98251	Abg98251 Human C-t	759	50	73.5	25	2	AAR40511	Aar40511 [D-Ala131
687	51	75.0	22	2	AAR25713	Aar25713 Atrial na	760	50	73.5	25	2	AAR40517	Aar40517 [D-Ala132
688	51	75.0	23	1	AAP70968	Aap70968 Sequence	761	50	73.5	25	2	AAR40518	Aar40518 [D-Ala132
689	51	75.0	23	1	AAP70969	Aap70969 Sequence	762	50	73.5	25	2	AAR40518	Aar40518 [D-Ala132
690	51	75.0	24	1	AAP70963	Aap70963 Sequence	763	50	73.5	25	2	AAR40512	Aar40512 [D-Ala135
691	51	75.0	24	1	AAP93041	Aap93041 Sequence	764	50	73.5	25	2	AAR40564	Aar40564 [Asn136]h
692	51	75.0	25	2	AAR40741	Aar40741 [Glu136]h	765	50	73.5	25	2	AAR40563	Aar40563 [Asn136]h
693	51	75.0	25	2	AAR40740	Aar40740 [Glu135]r	766	50	73.5	25	2	AAR40558	Aar40558 [Asn135]r
694	51	75.0	25	2	AAR42953	Aar42953 Polypepti	767	50	73.5	25	8	ADL22352	Adl22352 Natriuret
695	51	75.0	32	2	AAW51274	Aaw51274 Human B-t	768	50	73.5	25	8	ADL22356	Adl22356 Natriuret
696	51	75.0	32	3	AAY80244	Aay80244 Human B-t	769	50	73.5	25	8	ADL22355	Adl22355 Natriuret
697	50	73.5	17	5	ABG98210	Abg98210 Human C-t	770	50	73.5	25	8	ADP49282	Adp49282 Natriuret
698	50	73.5	17	5	ABG98249	Abg98249 Human C-t	771	50	73.5	26	3	ABU63216	Aay67295 Human bra
699	50	73.5	17	5	ABG98254	Abg98254 Human C-t	772	50	73.5	26	6	ADL22357	Adl22357 Natriuret
700	50	73.5	17	5	ABG98238	Abg98238 Human C-t	773	50	73.5	26	8	ADL22354	Adl22354 Natriuret
701	50	73.5	17	5	ABG98232	Abg98232 Human C-t	774	50	73.5	26	8	ADL22354	Adl22354 Natriuret
702	50	73.5	17	8	ADL22369	Adl22369 Natriuret	775	50	73.5	26	8	ADP49303	Adp49303 Natriuret
703	50	73.5	17	8	ADL22372	Adl22372 Natriuret	776	50	73.5	26	8	ADP49273	Adp49273 Natriuret
704	50	73.5	17	8	ADL22373	Adl22373 Natriuret	777	50	73.5	26	9	ADW45317	Adw45317 Human fus
705	50	73.5	17	8	ADL22370	Adl22370 Natriuret	778	50	73.5	26	9	ADY62994	Ady62994 Human bra
706	50	73.5	17	8	ADP49292	Adp49292 Natriuret	779	50	73.5	27	8	ADP49289	Adp49289 Natriuret
707	50	73.5	17	9	AE812959	Aeb12959 Human bra	780	50	73.5	27	9	ADW45318	Adw45318 Human fus
708	50	73.5	18	2	AAR40656	Aar40656 [Arg128]l	781	50	73.5	27	9	ADW45367	Adw45367 Human BNP
709	50	73.5	18	2	AAR40671	Aar40671 [Arg129]l	782	50	73.5	28	2	AAR14464	Aar14464 Atrial na
710	50	73.5	18	2	AAR40659	Aar40659 [Arg129]l	783	50	73.5	28	9	ADW45365	Adw45365 Human BNP
711	50	73.5	18	2	AAR40668	Aar40668 [Arg128]l	784	50	73.5	28	9	ADW45319	Adw45319 Human fus
712	50	73.5	18	8	ADL22374	Adl22374 Natriuret	785	50	73.5	29	1	AAP70972	Aap70972 Sequence
713	50	73.5	18	8	ADL22371	Adl22371 Natriuret	786	50	73.5	29	8	ADP49272	Adp49272 Natriuret
714	50	73.5	19	8	ADP49259	Adp49259 Natriuret	787	50	73.5	29	8	ADP49302	Adp49302 Natriuret
715	50	73.5	19	8	ADP49298	Adp49298 Natriuret	788	50	73.5	29	9	ADW45311	Adw45311 Human fus
716	50	73.5	20	2	AAR40516	Aar40516 [D-Ala131	789	50	73.5	30	9	ADW45310	Adw45310 Human fus
717	50	73.5	20	2	AAR40522	Aar40522 [D-Ala132	790	50	73.5	30	9	ADP49258	Adp49258 Natriuret
718	50	73.5	20	2	AAR40568	Aar40568 [Asn136]h	791	50	73.5	31	2	AAR34302	Aar34302 Mutated B
719	50	73.5	20	2	AAR40562	Aar40562 [Asn135]r	792	50	73.5	32	2	AAR40861	Aar40861 BNP. 3/19
720	50	73.5	21	2	AAR40667	Aar40667 [Arg128]l	793	50	73.5	32	2	AAR34301	Aar34301 Mutated h
721	50	73.5	21	2	AAR40658	Aar40658 [Arg129]l	794	50	73.5	32	2	AAR36381	Aar36381 Recombina
722	50	73.5	21	2	AAR40673	Aar40673 [Arg128]l	795	50	73.5	32	2	AAW70090	Aaw70090 Brain nat
723	50	73.5	21	2	AAR40670	Aar40670 [Arg129]l	796	50	73.5	32	2	AAW67040	Aaw67040 Brain nat
724	50	73.5	21	2	AAR40655	Aar40655 [Arg128]l	797	50	73.5	32	2	AAW51305	Aaw51305 Human B-t
725	50	73.5	22	1	AAP71038	Aap71038 Peptide w	798	50	73.5	32	2	AAW51278	Aaw51278 Human B-t
726	50	73.5	23	2	AAR40669	Aar40669 [Arg129]l	799	50	73.5	32	2	AAW51280	Aaw51280 Human B-t
727	50	73.5	23	2	AAR40654	Aar40654 [Arg128]l	799	50	73.5	32	3	AAW80250	Aay80250 Human B-t
728	50	73.5	23	2	AAR40666	Aar40666 [Arg129]l	801	50	73.5	32	3	AAW80213	Aay80213 Human B-t
729	50	73.5	23	2	AAR40657	Aar40657 [Arg129]l	802	50	73.5	32	3	AAW80248	Aay80248 Human B-t
730	50	73.5	23	2	AAR40672	Aar40672 [Arg128]l	803	50	73.5	32	4	AAB82550	Aab82550 Human bra
731	50	73.5	23	2	AAR40567	Aar40567 [Asn136]h	804	50	73.5	32	4	AAB91333	Aab91333 Brain nat
732	50	73.5	23	2	AAR40515	Aar40515 [D-Ala131	805	50	73.5	32	4	AAB91340	Aab91340 Brain nat
733	50	73.5	23	2	AAR40521	Aar40521 [D-Ala132	806	50	73.5	32	4	AAB45739	Aab45739 Human mat
734	50	73.5	23	2	AAR40561	Aar40561 [Asn135]r	807	50	73.5	32	4	AAE12434	Aae12434 Human bra
735	50	73.5	23	8	ADL22365	Adl22365 Natriuret	808	50	73.5	32	4	AAB70810	Aab70810 Human bra
736	50	73.5	23	8	ADL22362	Adl22362 Natriuret	809	50	73.5	32	5	ABG98205	Abg98205 Human bra
737	50	73.5	23	8	ADL22364	Adl22364 Natriuret	810	50	73.5	32	6	ADA00765	Ada00765 Human nat
738	50	73.5	23	8	ADL22361	Adl22361 Natriuret	811	50	73.5	32	6	ADA00784	Ada00784 Human bra
739	50	73.5	23	8	ADL22358	Adl22358 Natriuret	812	50	73.5	32	7	ABU63215	Abu63215 Human bra
740	50	73.5	23	8	ADL22359	Adl22359 Natriuret	813	50	73.5	32	7	ADD55931	Add55931 Human B-t
741	50	73.5	24	1	AAP70967	Aap70967 Sequence	814	50	73.5	32	7	ADD93296	Add93296 Human act
742	50	73.5	24	1	AAP94852	Aap94852 Sequence	815	50	73.5	32	7	ADF16700	Adf16700 Human alb
743	50	73.5	24	1	AAP93098	Aap93098 Sequence	816	50	73.5	32	8	ADJ79634	Adj79634 Human Bra
744	50	73.5	24	2	AAR40514	Aar40514 [D-Ala131	817	50	73.5	32	8	ADL22376	Adl22376 Natriuret
745	50	73.5	24	2	AAR40565	Aar40565 [Asn136]h	818	50	73.5	32	8	ADL22378	Adl22378 Natriuret
746	50	73.5	24	2	AAR40513	Aar40513 [D-Ala131	819	50	73.5	32	8	ADL22384	Adl22384 Natriuret
747	50	73.5	24	2	AAR40519	Aar40519 [D-Ala132	820	50	73.5	32	8	ADL22382	Adl22382 Natriuret
748	50	73.5	24	2	AAR40560	Aar40560 [Asn135]r	821	50	73.5	32	8	ADL22379	Adl22379 Natriuret
749	50	73.5	24	2	AAR40559	Aar40559 [Asn135]r	822	50	73.5	32	8	ADL22381	Adl22381 Natriuret
750	50	73.5	24	2	AAR40566	Aar40566 [Asn136]h	823	50	73.5	32	8	ADL22367	Adl22367 Natriuret
751	50	73.5	24	2	AAR40520	Aar40520 [D-Ala132	824	50	73.5	32	8	ADL22375	Adl22375 Natriuret
752	50	73.5	24	2	AAR37337	Aar37337 Atriopept	825	50	73.5	32	8	ADL22386	Adl22386 Natriuret
753	50	73.5	24	2	AAR37338	Aar37338 Atriopept	826	50	73.5	32	8	ADN03300	Adn03300 Exemplary
754	50	73.5	24	4	AAB46799	Aab46799 Human bra	827	50	73.5	32	8	ADN03300	Adn03300 Exemplary

828	50	73.5	32	8	ADP49307	Adp49307	Natriuret	901	50	73.5	175	2	AAR72812	Aar72812	Gamma-IFN
829	50	73.5	32	8	ADP49290	Adp49290	Natriuret	902	50	73.5	197	8	ADM57398	Adm57398	Protein P
830	50	73.5	32	8	ADP49308	Adp49308	Natriuret	903	50	73.5	630	9	ADM45230	Adm45230	Human inv
831	50	73.5	32	8	ADP49291	Adp49291	Natriuret	904	50	73.5	631	9	ADM45231	Adm45231	Human inv
832	50	73.5	32	8	ADR42135	Adr42135	BNP relat	905	50	73.5	632	9	ADM45232	Adm45232	Human inv
833	50	73.5	32	9	ADV86891	Adv86891	Human BNP	906	50	73.5	633	9	ADM45224	Adm45224	Human inv
834	50	73.5	32	9	ADM08061	Adm08061	Human bra	907	50	73.5	641	7	ADF16537	Adf16537	Human alb
835	50	73.5	32	9	ADW95867	Adw95867	Human bra	908	50	73.5	641	9	ADM45226	Adm45226	Human ser
836	50	73.5	32	9	ADM45284	Adm45284	Human fus	909	50	73.5	641	9	ADM45207	Adm45207	Human ser
837	50	73.5	32	9	ADM45314	Adm45314	Human fus	910	50	73.5	661	9	ADM45277	Adm45277	Human ser
838	50	73.5	32	9	ADM45294	Adm45294	Human fus	911	50	73.5	663	9	ADM45280	Adm45280	Human ser
839	50	73.5	32	9	ADM45366	Adm45366	Human BNP	912	50	73.5	665	9	ADM45278	Adm45278	Human ser
840	50	73.5	32	9	ADM45300	Adm45300	Human fus	913	50	73.5	667	9	ADM45223	Adm45223	Human ser
841	50	73.5	32	9	ADM45313	Adm45313	Human fus	914	50	73.5	670	9	ADM45279	Adm45279	Human ser
842	50	73.5	32	9	ADY62993	Ady62993	Human bra	915	50	73.5	673	9	ADM45197	Adm45197	Human ser
843	50	73.5	32	9	AEA53023	Aea53023	Protein q	916	50	73.5	673	9	ADM45213	Adm45213	Human ser
844	50	73.5	32	9	AEB63461	Aeb63461	HUMNATPEP	917	50	73.5	673	9	ADM45227	Adm45227	Human ser
845	50	73.5	33	2	AAR45762	Aar45762	GLU-BNP.	918	50	73.5	719	7	ADF16188	Adf16188	Human alb
846	50	73.5	33	2	AAR35490	Aar35490	Tyr-hBNP.	919	49	72.1	17	1	AAP71035	Aap71035	Peptide w
847	50	73.5	33	8	ADL22377	Adl22377	Natriuret	920	49	72.1	17	5	ABG98271	Abg98271	Human C-t
848	50	73.5	33	8	ADL22383	Adl22383	Natriuret	921	49	72.1	17	5	ABG98231	Abg98231	Human C-t
849	50	73.5	33	8	ADL22380	Adl22380	Natriuret	922	49	72.1	17	5	ABG98209	Abg98209	Human C-t
850	50	73.5	33	8	ADL22385	Adl22385	Natriuret	923	49	72.1	17	5	ABG98229	Abg98229	Human C-t
851	50	73.5	33	8	ADL22368	Adl22368	Natriuret	924	49	72.1	17	5	ABG98237	Abg98237	Human C-t
852	50	73.5	33	8	ADP49309	Adp49309	Natriuret	925	49	72.1	17	5	ABG98230	Abg98230	Human C-t
853	50	73.5	34	2	ADP49293	Adp49293	Natriuret	926	49	72.1	18	2	AAR40615	Aar40615	[Arg128] (
854	50	73.5	34	2	AAR45761	Aar45761	Leader-GL	927	49	72.1	18	2	AAR40662	Aar40662	[Arg128] (
855	50	73.5	35	4	AAB91330	Aab91330	Atrial-na	928	49	72.1	18	2	AAR40633	Aar40633	[Arg128] (
856	50	73.5	35	8	ADJ79736	Adj79736	Human Bra	929	49	72.1	18	2	AAR40618	Aar40618	[Arg129] (
857	50	73.5	41	4	AAB82543	Aab82543	Human bra	930	49	72.1	18	2	AAR40665	Aar40665	[Arg129] (
858	50	73.5	41	6	ABU63210	Abu63210	Chimeric	931	49	72.1	18	2	AAR40636	Aar40636	[Arg129] (
859	50	73.5	41	9	ADM08080	Adm08080	Human bra	932	49	72.1	20	2	AAR40422	Aar40422	[D-Ala132
860	50	73.5	41	9	ADY62988	Ady62988	Natriuret	933	49	72.1	20	2	AAR40701	Aar40701	[Ser135] r
861	50	73.5	42	9	AEB63459	Aeb63459	HUMNATPEP	934	49	72.1	20	2	AAR40719	Aar40719	[Leu130] r
862	50	73.5	52	9	ADM45364	Adm45364	Human BNP	935	49	72.1	20	2	AAR40546	Aar40546	[D-Cys130
863	50	73.5	60	9	ADW08083	Adw08083	Human bra	936	49	72.1	20	2	AAR40462	Aar40462	[D-Ala144
864	50	73.5	60	9	AEB63460	Aeb63460	HUMNATPEP	937	49	72.1	20	2	AAR40725	Aar40725	[Leu131] h
865	50	73.5	108	7	ADD93297	Add93297	Human pro	938	49	72.1	20	2	AAR40534	Aar40534	[D-Ala132
866	50	73.5	108	8	ADJ79633	Adj79633	Human Bra	939	49	72.1	20	2	AAR40540	Aar40540	[D-Cys129
867	50	73.5	108	8	ADO47364	Ado47364	Human bra	940	49	72.1	20	2	AAR40416	Aar40416	[D-Ala131
868	50	73.5	108	8	ADO32544	Ado32544	Human NT-	941	49	72.1	20	2	AAR40528	Aar40528	[D-Ala131
869	50	73.5	108	8	ADQ30871	Adq30871	Human pro	942	49	72.1	20	2	AAR40468	Aar40468	[D-Ala145
870	50	73.5	108	8	ADR75282	Adr75282	Human bra	943	49	72.1	20	2	AAR40707	Aar40707	[Ser136] h
871	50	73.5	108	8	ADS54316	Ads54316	Human B-t	944	49	72.1	21	1	AAP40849	Aap40849	Sequence
872	50	73.5	108	8	ADU05011	Adu05011	Amino aci	945	49	72.1	21	2	AAR40635	Aar40635	[Arg129] (
873	50	73.5	108	8	ADU04660	Adu04660	Human bra	946	49	72.1	21	2	AAR40664	Aar40664	[Arg129] (
874	50	73.5	108	9	ADW95866	Adw95866	Human pro	947	49	72.1	21	2	AAR40617	Aar40664	[Arg129] (
875	50	73.5	108	9	ADY34277	Ady34277	Human bra	948	49	72.1	21	2	AAR40661	Aar40661	[Arg128] (
876	50	73.5	108	9	ADZ22717	Adz22717	Human B-t	949	49	72.1	21	2	AAR40614	Aar40614	[Arg128] (
877	50	73.5	109	4	AA845738	Aa845738	Human BNP	950	49	72.1	21	2	AAP40632	Aar40632	[Arg128] (
878	50	73.5	117	8	ADM57402	Adm57402	Protein p	951	49	72.1	22	1	AAP71372	Aap71372	Antinyper
879	50	73.5	118	6	ABR96183	Ab96183	Human NOV	952	49	72.1	22	2	AAR25743	Aar25743	Actrial na
880	50	73.5	121	8	ADM57400	Adm57400	Protein p	953	49	72.1	22	2	AAR29775	Aar29775	Actrial na
881	50	73.5	129	9	AEB63486	Aeb63486	HUMNATPEP	954	49	72.1	22	2	AAR29776	Aar29776	Actrial na
882	50	73.5	134	2	AAR06603	Aar06603	Human Bra	955	49	72.1	23	2	AAR40527	Aar40527	[D-Ala131
883	50	73.5	134	2	AAR04087	Aar04087	Protein e	956	49	72.1	23	2	AAR40533	Aar40533	[D-Ala132
884	50	73.5	134	2	AAy05325	Aay05325	Human gam	957	49	72.1	23	2	AAR40718	Aar40718	[Leu130] r
885	50	73.5	134	4	AA845735	Aab45735	Human BNP	958	49	72.1	23	2	AAR40700	Aar40700	[Ser135] r
886	50	73.5	134	7	ADD93293	Add93293	Human pre	959	49	72.1	23	2	AAR36970	Aar36970	ANVP #34.
887	50	73.5	134	7	ADP16190	Adf16190	Human alb	960	49	72.1	23	2	AAR40461	Aar40461	[D-Ala144
888	50	73.5	134	7	ADU05012	Adu05012	Amino aci	961	49	72.1	23	2	AAR40556	Aar40556	[D-Ala132
889	50	73.5	134	8	ADM41413	Adm41413	Human bra	962	49	72.1	23	2	AAR40524	Aar40524	[Leu131] h
890	50	73.5	134	8	ADQ30872	Adq30872	Human pre	963	49	72.1	23	2	AAR36968	Aar36968	ANVP #32.
891	50	73.5	134	8	ADR75283	Adr75283	Human bra	964	49	72.1	23	2	AAR40551	Aar40551	[D-Ala131
892	50	73.5	134	8	ADS54317	Ad54317	Human B-t	965	49	72.1	23	2	AAR40660	Aar40660	[Arg128] (
893	50	73.5	134	8	ADU04661	Adu04661	Human bra	966	49	72.1	23	2	AAR40415	Aar40415	[D-Ala131
894	50	73.5	134	9	ADY34278	Ady34278	Human bra	967	49	72.1	23	2	AAR40634	Aar40634	[Arg129] (
895	50	73.5	134	9	ADZ22718	Adz22718	Human pre	968	49	72.1	23	2	AAR40663	Aar40663	[Arg129] (
896	50	73.5	134	9	AEB63456	Aeb63456	HUMNATPEP	969	49	72.1	23	2	AAR40613	Aar40613	[Arg128] (
897	50	73.5	143	9	ADM08049	Adm08049	Human bra	970	49	72.1	23	2	AAR40467	Aar40467	[D-Ala145
898	50	73.5	143	9	ADW08048	Adw08048	Human bra	971	49	72.1	23	2	AAR40539	Aar40539	[D-Cys129
899	50	73.5	162	9	AEB63457	Aeb63457	HUMNATPEP	972	49	72.1	23	2	AAR40545	Aar40545	[D-Cys130
900	50	73.5	162	9	AEB63457	Aeb63457	HUMNATPEP	973	49	72.1	23	2	AAR40545	Aar40545	[D-Cys130

974	49	72.1	23	2	AAR40421	Aar40421	[D-Ala132
975	49	72.1	23	2	AAR40616	Aar40616	[Arg129]l
976	49	72.1	23	2	AAR40631	Aar40631	[Arg128]l
977	49	72.1	23	2	AAR40706	Aar40706	[Ser136]h
978	49	72.1	23	2	AAR40552	Aar40552	[D-Ala132
979	49	72.1	24	1	AAE50908	Aap50908	Sequence
980	49	72.1	24	2	AAR40544	Aar40544	[D-Cys130
981	49	72.1	24	2	AAR40513	Aar40413	[D-Ala131
982	49	72.1	24	2	AAR40531	Aar40531	[D-Ala132
983	49	72.1	24	2	AAR40550	Aar40550	[D-Ala131
984	49	72.1	24	2	AAR40704	Aar40704	[Ser136]h
985	49	72.1	24	2	AAR40538	Aar40538	[D-Cys129
986	49	72.1	24	2	AAR40716	Aar40716	[Leu130]r
987	49	72.1	24	2	AAR40526	Aar40526	[D-Ala131
988	49	72.1	24	2	AAR40698	Aar40698	[Ser135]r
989	49	72.1	24	2	AAR40723	Aar40723	[Leu131]h
990	49	72.1	24	2	AAR40717	Aar40717	[Leu130]r
991	49	72.1	24	2	AAR40525	Aar40525	[D-Ala131
992	49	72.1	24	2	AAR40532	Aar40532	[D-Ala132
993	49	72.1	24	2	AAE40699	Aar40699	[Ser135]r
994	49	72.1	24	2	AAR40705	Aar40705	[Ser136]h
995	49	72.1	24	2	AAR40414	Aar40414	[D-Ala131
996	49	72.1	24	2	AAE40419	Aar40419	[D-Ala132
997	49	72.1	24	2	AAE40459	Aar40459	[D-Ala144
998	49	72.1	24	2	AAE40465	Aar40465	[D-Ala145
999	49	72.1	24	2	AAE40554	Aar40554	[D-Ala132
1000	49	72.1	24	2	AAE40420	Aar40420	[D-Ala132

ALIGNMENTS

RESULT 1	
ID	ABG98259 standard; peptide; 17 AA.
XX	
AC	ABG98259;
XX	
DT	08-JAN-2003 (first entry)
XX	
DE	Human C-type natriuretic peptide (CNP) variant #53.
XX	
KW	Human; natriuretic peptide; NP; endochondral ossification;
KW	bone formation; cartilage; bone; signalling pathway; FGF;
KW	fibroblast growth factor; cardiovascular homeostasis; diuresis;
KW	natriuresis; vasodilation; atrial natriuretic peptide; ANP;
KW	brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
KW	dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
KW	guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
KW	skeletal dysplasia; achondroplasia; osteopathic.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200274234-A2.
XX	
PD	26-SEP-2002.
XX	
PF	20-MAR-2002; 2002WO-IL000229.
XX	
PR	20-MAR-2001; 2001IL-00142118.
PR	20-MAR-2001; 2001US-0276939P.
XX	
PA	(PROC-) PROCHON BIOTECH LTD.
XX	
PI	Golembo M, Yayon A;
XX	
DR	WPI; 2002-750515/81.
XX	
PT	Pharmaceutical composition useful in the treatment of skeletal dysplasias
PT	e.g. achondroplasia comprises at least one natriuretic peptide.
XX	
PS	Example 6; Page 23; 41pp; English.

XX	
CC	The invention discloses a pharmaceutical composition comprising at least
CC	one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC	Endochondral ossification is a fundamental mechanism for bone formation,
CC	whereby cartilage is replaced by bone. Endochondral ossification is the
CC	result of the concerted action of several signalling pathways, most
CC	notably the pathway triggered by the activation of the fibroblast growth
CC	factor (FGF). Natriuretic peptides are also known for their role in
CC	cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
CC	isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
CC	peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
CC	natriuretic peptide (DNP). NP's effect their biological role through two
CC	receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
CC	which are activated upon ligand binding and lead to accumulation of
CC	intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
CC	inhibition of the NEPs increases the concentration of the NPs in the
CC	circulation. The invention discloses compositions comprising NP secreting
CC	cells and methods for treating skeletal dysplasias involving
CC	transplanting or implanting the natriuretic peptide secreting cells. The
CC	NP secreting cells are useful in the manufacture of a medicament for the
CC	treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
CC	abnormal bone and for increasing the size of bone growth plate in
CC	abnormal bone (e.g. limb bone). The compositions induce bone elongation
CC	in abnormal bone growth and enhance NP stabilisation in circulation. The
CC	sequences presented in ABG98202-ABG98272 are the CNP peptide and
CC	variants, with differing levels of activity, designed from it. The
CC	degenerate peptide is presented in ABG98206
XX	
SQ	Sequence 17 AA;

Query Match 82.4%; Score 56; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	1	CFGXXXDRIGXXSXXGC	17
Db	1	CFGUKLDRIQSMALGC	17

RESULT 2	
ABG98264	
ID	ABG98264 standard; peptide; 17 AA.
XX	
AC	ABG98264;
XX	
DT	08-JAN-2003 (first entry)
XX	
DE	Human C-type natriuretic peptide (CNP) variant #58.
XX	
KW	Human; natriuretic peptide; NP; endochondral ossification;
KW	bone formation; cartilage; bone; signalling pathway; FGF;
KW	fibroblast growth factor; cardiovascular homeostasis; diuresis;
KW	natriuresis; vasodilation; atrial natriuretic peptide; ANP;
KW	brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
KW	dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
KW	guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
KW	skeletal dysplasia; achondroplasia; osteopathic.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200274234-A2.
XX	
PD	26-SEP-2002.
XX	
PF	20-MAR-2002; 2002WO-IL000229.
XX	
PR	20-MAR-2001; 2001IL-00142118.
PR	20-MAR-2001; 2001US-0276939P.
XX	
PA	(PROC-) PROCHON BIOTECH LTD.
XX	
PI	Golembo M, Yayon A;

XX WPI; 2002-750515/81.
DR
XX Pharmaceutical composition useful in the treatment of skeletal dysplasias
PT e.g. achondroplasia comprises at least one natriuretic peptide.
XX
XX Example 6; Page 23; 41pp; English.
PS
CC The invention discloses a pharmaceutical composition comprising at least
CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC Endochondral ossification is a fundamental mechanism for bone formation,
CC whereby cartilage is replaced by bone. Endochondral ossification is the
CC result of the concerted action of several signalling pathways, most
CC notably the pathway triggered by the activation of the fibroblast growth
CC factor (FGF). Natriuretic peptides are also known for their role in
CC cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
CC natriuretic peptide (DNP). NP's effect their biological role through two
CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
CC which are activated upon ligand binding and lead to accumulation of
CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
CC inhibition of the NEPs increases the concentration of the NPs in the
CC circulation. The invention discloses compositions comprising NP secreting
CC cells and methods for treating skeletal dysplasias involving NP
CC transplanting or implanting the natriuretic peptide secreting cells. The
CC NP secreting cells are useful in the manufacture of a medicament for the
CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
CC abnormal bone and for increasing the size of bone growth plate in
CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
CC in abnormal bone growth and enhance NP stabilisation in circulation. The
CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
CC variants, with differing levels of activity, designed from it. The
CC degenerate peptide is presented in ABG98206
XX
SQ Sequence 17 AA:

Query Match 82.4%; Score 56; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
Db 1 CFGKLDRIGSMGAGC 17

RESULT 3
ABG98241 standard; peptide; 17 AA.
ID
XX
AC ABG98241;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human C-type natriuretic peptide (CNP) variant #35.
XX
KW Human; natriuretic peptide; NP; endochondral ossification;
KW bone formation; cartilage; bone; signalling pathway; FGF;
KW fibroblast growth factor; cardiovascular homeostasis; diuresis;
KW natriuresis; vasodilation; atrial natriuretic peptide; ANP;
KW brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
KW dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
KW guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
KW skeletal dysplasia; achondroplasia; osteopathic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200274234-A2.
XX
XX 26-SEP-2002.
PD
XX
PF 20-MAR-2002; 2002WO-IL000229.

XX 20-MAR-2001; 2001IL-00142118.
PR
PR 20-MAR-2001; 2001US-0276939P.
XX
XX (PROC-) PROCHON BIOTECH LTD.
PA
XX
PI Golemo M, Yayon A;
PI
XX
XX WPI; 2002-750515/81.
DR
XX
XX Pharmaceutical composition useful in the treatment of skeletal dysplasias
PT e.g. achondroplasia comprises at least one natriuretic peptide.
XX
XX Example 6; Page 23; 41pp; English.
PS
CC The invention discloses a pharmaceutical composition comprising at least
CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC Endochondral ossification is a fundamental mechanism for bone formation,
CC whereby cartilage is replaced by bone. Endochondral ossification is the
CC result of the concerted action of several signalling pathways, most
CC notably the pathway triggered by the activation of the fibroblast growth
CC factor (FGF). Natriuretic peptides are also known for their role in
CC cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
CC natriuretic peptide (DNP). NP's effect their biological role through two
CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
CC which are activated upon ligand binding and lead to accumulation of
CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
CC inhibition of the NEPs increases the concentration of the NPs in the
CC circulation. The invention discloses compositions comprising NP secreting
CC cells and methods for treating skeletal dysplasias involving NP
CC transplanting or implanting the natriuretic peptide secreting cells. The
CC NP secreting cells are useful in the manufacture of a medicament for the
CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
CC abnormal bone and for increasing the size of bone growth plate in
CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
CC in abnormal bone growth and enhance NP stabilisation in circulation. The
CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
CC variants, with differing levels of activity, designed from it. The
CC degenerate peptide is presented in ABG98206
XX
SQ Sequence 17 AA:

Query Match 82.4%; Score 56; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
Db 1 CFGAKLDRIGSMGLGC 17

RESULT 4
ABG98246 standard; peptide; 17 AA.
ID
XX
AC ABG98246;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human C-type natriuretic peptide (CNP) variant #40.
XX
KW Human; natriuretic peptide; NP; endochondral ossification;
KW bone formation; cartilage; bone; signalling pathway; FGF;
KW fibroblast growth factor; cardiovascular homeostasis; diuresis;
KW natriuresis; vasodilation; atrial natriuretic peptide; ANP;
KW brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
KW dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
KW guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
KW skeletal dysplasia; achondroplasia; osteopathic.
XX
OS Homo sapiens.
OS

OS Synthetic.
XX
PN WO200274234-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-IL000229.
XX
PR 20-MAR-2001; 2001IL-00142118.
PR 20-MAR-2001; 2001US-0276939P.
XX
PA (PROC-) PROCHON BIOTECH LTD.
XX
PI Golembo M, Yayon A;
XX
DR WPI; 2002-750515/81.
XX
PT Pharmaceutical composition useful in the treatment of skeletal dysplasias
PT e.g. achondroplasia comprises at least one natriuretic peptide.
XX
XX Example 6; Page 23; 41pp; English.
XX
CC The invention discloses a pharmaceutical composition comprising at least
CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC Endochondral ossification is a fundamental mechanism for bone formation,
CC whereby cartilage is replaced by bone. Endochondral ossification is the
CC result of the concerted action of several signalling pathways, most
CC notably the pathway triggered by the activation of the fibroblast growth
CC factor (FGF). Natriuretic peptides are also known for their role in
CC cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
CC natriuretic peptide (DNP). NP's effect their biological role through two
CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
CC which are activated upon ligand binding and lead to accumulation of
CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
CC inhibition of the NEPs increases the concentration of the NPs in the
CC circulation. The invention discloses compositions comprising NP secreting
CC cells and methods for treating skeletal dysplasias involving
CC transplanting or implanting the natriuretic peptide secreting cells. The
CC NP secreting cells are useful in the manufacture of a medicament for the
CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
CC abnormal bone and for increasing the size of bone growth plate in
CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
CC in abnormal bone growth and enhance NP stabilisation in circulation. The
CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
CC variants, with differing levels of activity, designed from it. The
CC degenerate peptide is presented in ABG98206
XX
SQ Sequence 17 AA;

Query Match 82.4%; Score 56; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXGXC 17
||| ||||| |
Db 1 CFGLKADRIGSMGSLGC 17

RESULT 5
ABG98269
ID ABG98269 standard; peptide; 17 AA.
XX
AC ABG98269;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human C-type natriuretic peptide (CNP) variant #63.
XX
KW Human; natriuretic peptide; NP; endochondral ossification;
KW bone formation; cartilage; bone; signalling pathway; FGF;
KW fibroblast growth factor; cardiovascular homeostasis; diuresis;

KW natriuresis; vasodilation; atrial natriuretic peptide; ANP;
KW brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
KW dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
KW guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
KW skeletal dysplasia; achondroplasia; osteopathic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200274234-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-IL000229.
XX
PR 20-MAR-2001; 2001IL-00142118.
PR 20-MAR-2001; 2001US-0276939P.
XX
PA (PROC-) PROCHON BIOTECH LTD.
XX
PI Golembo M, Yayon A;
XX
DR WPI; 2002-750515/81.
XX
PT Pharmaceutical composition useful in the treatment of skeletal dysplasias
PT e.g. achondroplasia comprises at least one natriuretic peptide.
XX
XX Example 6; Page 23; 41pp; English.
XX
CC The invention discloses a pharmaceutical composition comprising at least
CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC Endochondral ossification is a fundamental mechanism for bone formation,
CC whereby cartilage is replaced by bone. Endochondral ossification is the
CC result of the concerted action of several signalling pathways, most
CC notably the pathway triggered by the activation of the fibroblast growth
CC factor (FGF). Natriuretic peptides are also known for their role in
CC cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
CC natriuretic peptide (DNP). NP's effect their biological role through two
CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
CC which are activated upon ligand binding and lead to accumulation of
CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
CC inhibition of the NEPs increases the concentration of the NPs in the
CC circulation. The invention discloses compositions comprising NP secreting
CC cells and methods for treating skeletal dysplasias involving
CC transplanting or implanting the natriuretic peptide secreting cells. The
CC NP secreting cells are useful in the manufacture of a medicament for the
CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
CC abnormal bone and for increasing the size of bone growth plate in
CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
CC in abnormal bone growth and enhance NP stabilisation in circulation. The
CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
CC variants, with differing levels of activity, designed from it. The
CC degenerate peptide is presented in ABG98206
XX
SQ Sequence 17 AA;

Query Match 82.4%; Score 56; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXGXC 17
||| ||||| |
Db 1 CFGLKLDRISSSGSLGC 17

RESULT 6
ABG98211
ID ABG98211 standard; peptide; 17 AA.
XX
AC ABG98211;
XX

DT 08-JAN-2003 (first entry)
XX
DE Human C-type natriuretic peptide (CNP) variant #5.
XX
KW Human; natriuretic peptide; NP; endochondral ossification;
KW bone formation; cartilage; bone; signalling pathway; FGF;
KW fibroblast growth factor; cardiovascular homeostasis; diuresis;
KW natriuresis; vasodilation; atrial natriuretic peptide; ANP;
KW brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
KW dendraaspis natriuretic peptide; DNP; NPR-A; NPR-B;
KW guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
KW skeletal dysplasia; achondroplasia; osteopathic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200274234-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-IL000229.
XX
PR 20-MAR-2001; 2001JP-00142118.
PR 20-MAR-2001; 2001US-0276939P.
XX
PA (PROC-) PROCHON BIOTECH LTD.
XX
PI Golembo M, Yayon A;
XX
DR WPI; 2002-750515/81.
XX
PT Pharmaceutical composition useful in the treatment of skeletal dysplasias
PT e.g. achondroplasia comprises at least one natriuretic peptide.
XX
PS Example 6; Page 22; 41pp; English.
XX
CC The invention discloses a pharmaceutical composition comprising at least
CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC Endochondral ossification is a fundamental mechanism for bone formation,
CC whereby cartilage is replaced by bone. Endochondral ossification is the
CC result of the concerted action of several signalling pathways, most
CC notably the pathway triggered by the activation of the fibroblast growth
CC factor (FGF). Natriuretic peptides are also known for their role in
CC cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendraaspis
CC natriuretic peptide (DNP). NP's effect their biological role through two
CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
CC which are activated upon ligand binding and lead to accumulation of
CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
CC inhibition of the NEPs increases the concentration of the NPs in the
CC circulation. The invention discloses compositions comprising NP secreting
CC cells and methods for treating skeletal dysplasias involving
CC transplanting or implanting the natriuretic peptide secreting cells. The
CC NP secreting cells are useful in the manufacture of a medicament for the
CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
CC abnormal bone and for increasing the size of bone growth plate in
CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
CC in abnormal bone growth and enhance NP stabilisation in circulation. The
CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
CC variants, with differing levels of activity, designed from it. The
CC degenerate peptide is presented in ABG98206
XX
SQ Sequence 17 AA;

Query Match 82.4%; Score 56; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| |
DB 1 CFGKLDRIGSASGLGC 17

RESULT 7
AAR40630
ID AAR40630 standard; protein; 18 AA.
XX
AC AAR40630;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg129] [D-Ala143] hANVP (130-146) -NH2.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 2..18
FT Misc-difference 15
FT /note= "D form residue"
FT Modified-site 18
FT /note= "Amidated C terminal"
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 48; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 18 AA;

Query Match 82.4%; Score 56; DB 2; Length 18;
Best Local Similarity 58.8%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| |
DB 2 CFGGRMDRIGAQSALGC 18

RESULT 8
AAR40624
ID AAR40624 standard; protein; 18 AA.
XX
AC AAR40624;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg129] [D-Ala133] hANVP (130-146) -NH2.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Disulfide-bond 2. .18
FT Misc-difference 5 /note= "D form residue"
FT Modified-site 18 /note= "Amidated C terminal"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 47; 45pp; English.
XX
XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 18 AA;
QY 1 CFGXXXDRIGXXSXGC 17
Db 2 CFGARMDRIGAQSGLGC 18
RESULT 9
AAR40627
ID AAR40627 standard; protein; 18 AA.
XX
XX AAR40627;
AC
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg128] [D-Ala142] rANVP (129-145)-NH2.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 2. .18
FT Misc-difference 15 /note= "D form residue"
FT Modified-site 18

FT /note= "Amidated C terminal"
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 47; 45pp; English.
XX
XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 18 AA;
QY 1 CFGXXXDRIGXXSXGC 17
Db 2 CFGGRIDRIGAQSALGC 18

RESULT 10
AAR40621
ID AAR40621 standard; protein; 18 AA.
XX
XX AAR40621;
AC
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg128] [D-Ala132] rANVP (129-145)-NH2.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 2. .18
FT Misc-difference 5 /note= "D form residue"
FT Modified-site 18 /note= "Amidated C terminal"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.
PA
XX
XX Lewicki JA, Scarborough RM;
PI
XX WPI; 1993-175525/21.
DR
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
XX
PS Disclosure; Col 47; 45pp; English.
XX
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
CC
XX
SQ Sequence 18 AA;

Query Match 82.4%; Score 56; DB 2; Length 18;
Best Local Similarity 58.8%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFCGXXDRIGXXSXGC 17
Db 2 CFCGARIDRIGAQSGLGC 18

RESULT 11
AAR40455
ID AAR40455 standard; protein; 20 AA.
XX
XX AAR40455;
AC
XX 25-MAR-2003 (revised)
DT
DT 14-SEP-1993 (first entry)
XX
XX [D-Ala143]rANVP(127-146)-NH2.
DE
XX
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
KM
XX
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4..20
FT Misc-difference 17 /note= "D-form residue"
FT Modified-site 20 /note= "Amidated C-terminal"
FT
XX
XX US5212286-A.
PN
XX
XX 18-MAY-1993.
PD
XX
XX 05-JUN-1986; 86US-00870795.
PF
XX
XX 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
XX Lewicki JA, Scarborough RM;
PI
XX WPI; 1993-175525/21.
DR
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 34; 45pp; English.

XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
CC
XX
SQ Sequence 20 AA;

Query Match 82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFCGXXDRIGXXSXGC 17
Db 4 CFCGRMDRIGAQSALGC 20

RESULT 12
AAR40449
ID AAR40449 standard; protein; 20 AA.
XX
XX AAR40449;
AC
XX 25-MAR-2003 (revised)
DT
DT 14-SEP-1993 (first entry)
XX
XX [D-Ala142]rANVP(126-145)-NH2.
DE
XX
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
KM
XX
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4..20
FT Misc-difference 17 /note= "D-form residue"
FT Modified-site 20 /note= "Amidated C-terminal"
FT
XX
XX US5212286-A.
PN
XX
XX 18-MAY-1993.
PD
XX
XX 05-JUN-1986; 86US-00870795.
PF
XX
XX 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
XX Lewicki JA, Scarborough RM;
PI
XX WPI; 1993-175525/21.
DR
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
XX Disclosure; Col 33; 45pp; English.
PS
XX
XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
CC
XX
SQ Sequence 20 AA;

Query Match 82.4%; Score 56; DB 2; Length 20;

Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| |||| | ||
Db 4 CFGGRIDRIGAQSALGC 20

RESULT 13
AAR40434
ID AAR40434 standard; protein; 20 AA.
XX
AC AAR40434;
XX

XX 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX

DE [D-Ala133]ANVP(127-146)-NH2.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX

OS Synthetic.

XX Key Location/Qualifiers
FH Disulfide-bond 4..20
FT Misc-difference 7
FT Modified-site 20 /note= "D-form residue"
FT /note= "Amidated C-terminal"

XX US5212286-A.

XX 18-MAY-1993.

XX 05-JUN-1986; 86US-00870795.

XX 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.

XX PI Lewicki JA, Scarborough RM;

DR WPI; 1993-175525/21.

XX PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

PT in mammals.

XX PS Disclosure; Col 32; 45pp; English.

XX CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 20 AA;

Query Match 82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| |||| | ||
Db 4 CFGARMDRIGAQSGLGC 20

RESULT 14
AAR40454
ID AAR40454 standard; protein; 20 AA.

XX AAR40454;
AC
XX

XX 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX

DE [D-Ala143]rANVP(127-149)-NH2.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX

OS Synthetic.

XX Key Location/Qualifiers
FH Disulfide-bond 4..20
FT Misc-difference 17
FT Modified-site 20 /note= "D-form residue"
FT /note= "Amidated C-terminal"

XX US5212286-A.

XX 18-MAY-1993.

XX 05-JUN-1986; 86US-00870795.

XX 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.

XX PI Lewicki JA, Scarborough RM;

DR WPI; 1993-175525/21.

XX PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

PT in mammals.

XX PS Disclosure; Col 33; 45pp; English.

XX CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 20 AA;

Query Match 82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| |||| | ||
Db 4 CFGGRMDRIGAQSALGC 20

RESULT 15
AAR40428
ID AAR40428 standard; protein; 20 AA.
XX
AC AAR40428;
XX

XX 25-MAR-2003 (revised)

DT 14-SEP-1993 (first entry)

DE [D-Ala132]rANVP(126-145)-NH2.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX

RESULT 14
AAR40454
ID AAR40454 standard; protein; 20 AA.

OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4..20
FT Misc-difference 7 /note= "D-form residue"
FT Modified-site 20 /note= "Amidated C-terminal"
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 31; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 20 AA;

Query Match 82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
DB 4 CFGARIDRIGAQSGLGC 20

RESULT 16
AAB91293
ID AAB91293 standard; peptide; 20 AA.
XX
AC AAB91293;
XX
DT 22-JUN-2001 (first entry)
XX
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:469.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K,
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 352; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 20 AA;

Query Match 82.4%; Score 56; DB 4; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
DB 1 CFGSRIDRIGAQSGMGC 17

RESULT 17
AAB05585
ID AAB05585 standard; peptide; 20 AA.
XX
AC AAB05585;
XX
DT 22-APR-2002 (first entry)
XX
DE Dithiol peptide #13.
XX
KW Dithiol; disulfide bond; chemical reagent; sulphydryl group; SH group;
KW trans-(Pt(ethylenediamine)2Cl2)2+.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 4 /note= "amidated"
FT
XX
PN WO200192466-A2.
XX
PD 06-DEC-2001.
XX
PF 16-MAY-2001; 2001WO-US015923.
XX
PR 26-MAY-2000; 2000US-00579883.
XX
PA (REGC) UNIV CALIFORNIA.

PI Rabenstein DA, Shi T;
XX
DR WPI; 2002-114335/15.
XX
PT Forming an intramolecular disulfide bond in a peptide, comprises
PT contacting a peptide comprising at least two sulphydryl groups with an
PT oxidizing agent that forms disulfide linkages in peptides.
XX
PS Example 1; Page 15; 40pp; English.
XX
CC The present invention describes a method of forming an intramolecular
CC disulfide bond in a peptide, comprising contacting a peptide comprising
CC at least two sulphydryl (SH) groups with a compound (trans-
CC (Pt(ethylenediamine)2Cl2)2+) (I). Also describes are: (1) a solution (II)
CC comprising a peptide which comprises at least two sulfur groups, and (I);
CC (2) a peptide synthesiser (III) for the synthesis of a peptide having an
CC intramolecular disulfide linkage, comprises a number of vials containing
CC amino acids derivatised for chemical peptide synthesis, where at least
CC one of the vials comprises an amino acid that, when fully deprotected,
CC bears a SH group, and a vial comprising (I); (3) chemically synthesising
CC a peptide comprising a disulfide linkage, involving chemically coupling a
CC number of amino acids to form a peptide comprising at least two SH
CC groups, and contacting the peptide with (I); and (4) a kit for forming an
CC intramolecular disulfide bond in a peptide, comprises a container
CC containing (I). The method can be used for forming an intramolecular
CC disulfide bond in a peptide. (II) is useful as a positive control when
CC evaluating the efficacy of particular reagent species, and as a sample
CC solution when optimising a purification protocol to clean up or to
CC isolate the desired reaction product (e.g., when optimising a high
CC pressure liquid chromatography (HPLC) protocol or evaluating a particular
CC chromatography column). The present sequence represents a dithiol peptide
CC which is used in an example from the present invention
XX
SQ Sequence 20 AA;

Query Match 82.4%; Score 56; DB 5; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 1 CFGSRIDRIGAQSGMGC 17

RESULT 18
AAR03304
ID AAR03304 standard; protein; 21 AA.
XX
AC AAR03304;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 15-AUG-1990 (first entry)
XX
DE fANP-21 frog atrial natriuretic peptide.
XX
KW Atrial natriuretic peptide; fANP-21; diuretic; hypertensive.
XX
OS Rana catesbeiana.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..17
XX
PN JP02025500-A.
XX
PD 26-JAN-1990.
XX
PF 14-JUL-1988; 88JP-00173740.
XX
PR 14-JUL-1988; 88JP-00173740.
XX
PA (MATS/) MATSUO T.
XX

DR WPI; 1990-071805/10.
XX
XX New peptide with physiological activity - obtd. from heart of frog, has
PT diuretic and antihypertensive properties.
PT
XX
PS Claim 1; Fig 3; 8pp; Japanese.
XX
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 21 AA;

Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 1 CFGSRIDRIGAQSGMGC 17

RESULT 19
AAR40629
ID AAR40629 standard; protein; 21 AA.
XX
AC AAR40629;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg129] [D-Ala143] hANVP (130-149) -NH2.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX

OS Synthetic.

FH Key Location/Qualifiers
FT Disulfide-bond 2..18
FT Misc-difference 15 /note= "D form residue"
FT Modified-site 21 /note= "Amidated C terminal"
FT
XX
XX

US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 48; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 21 AA;

Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||| |
Db 2 CFGGRMDRIGAQSALGC 18

RESULT 20
AAR40620
ID AAR40620 standard; protein; 21 AA.

AC AAR40620;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg128] [D-Ala132] rANVP (129-148) -NH2.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 2..18
FT Misc-difference 5 /note= "D form residue"
FT Modified-site 21 /note= "Amidated C terminal"

XX US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.

XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.

XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX

PS Disclosure; Col 47; 45pp; English.

XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX

SQ Sequence 21 AA;

Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||| |
Db 2 CFGARIDRIGAQSGLGC 18

RESULT 21

AAR40623
ID AAR40623 standard; protein; 21 AA.
XX
AC AAR40623;

XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg129] [D-Ala133] hANVP (130-149) -NH2.

XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 2..18
FT Misc-difference 5 /note= "D form residue"
FT Modified-site 21 /note= "Amidated C terminal"

XX
PN US5212286-A.
XX
PD 18-MAY-1993.

XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.

XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.

XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX

PS Disclosure; Col 47; 45pp; English.

XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX

SQ Sequence 21 AA;

Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||| |
Db 2 CFGARMDRIGAQSGLGC 18

RESULT 22

AAR40626
ID AAR40626 standard; protein; 21 AA.

XX
AC AAR40626;

XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX

DE [Arg128] [D-Ala142] rANVP (129-148) -NH2.

XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;

KW regulation; fluid volume; blood pressure.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Disulfide-bond 2..18
FT Misc-difference 15 /note= "D form residue"
FT Modified-site 21 /note= "Amidated C terminal"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 47; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
CC
XX
SQ Sequence 21 AA;
QY
Db 1 CFGXXXXRIGXXSXXGC 17
2 CFGGRIDRIGAQSALGC 18
Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
RESULT 23
AAB91294
ID AAB91294 standard; peptide; 21 AA.
XX
AC AAB91294;
XX
DT 22-JUN-2001 (first entry)
XX
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:470.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX

PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 352; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 21 AA;
QY
Db 1 CFGXXXXRIGXXSXXGC 17
1 CFGSRIDRIGAQSGMGC 17
Query Match 82.4%; Score 56; DB 4; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
RESULT 24
AAR40448
ID AAR40448 standard; protein; 23 AA.
XX
AC AAR40448;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [D-Ala142] rANVP (126-148)-NH2.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4..20
FT Misc-difference 17 /note= "D-form residue"
FT Modified-site 23 /note= "Amidated C-terminal"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX

PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 33; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 23 AA;

Query Match 82.4%; Score 56; DB 2; Length 23;
Best Local Similarity 58.8%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 4 CFGGRIDRIGAGSALGC 20

RESULT 25
AAR36975
ID AAR36975 standard; protein; 23 AA.
XX
AC AAR36975;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE ANVP #39.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Disulfide-bond 2..18
FT Misc-difference 5 /note= "D-form residue"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX

PS Disclosure; Col 11; 45pp; English.
XX
CC The sequences given in AAR36937-78 are atrial natriuretic/vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR40387-749.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 23 AA;

Query Match 82.4%; Score 56; DB 2; Length 23;
Best Local Similarity 58.8%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 2 CFGARIDRIGAGSGLGC 18

RESULT 26
AAR36964
ID AAR36964 standard; protein; 23 AA.
XX
AC AAR36964;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE ANVP #28.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Disulfide-bond 2..18
FT Misc-difference 15 /note= "D-form residue"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 10; 45pp; English.
XX
CC The sequences given in AAR36937-78 are atrial natriuretic/vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR40387-749.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 23 AA;

Query Match 82.4%; Score 56; DB 2; Length 23;
Best Local Similarity 58.8%; Pred. No. 0.00046;

Matches	10;	Conservative	0;	Mismatches	7;	Indels	0;	Gaps	0;
QY	1	CFGXXXDRIGXXSXGC	17						
DB	2	CFGGRIDRIGAQSALGC	18						
RESULT 27									
ID	AAR40427	standard; protein; 23 AA.							
AC	AAR40427;								
XX									
DT	25-MAR-2003	(revised)							
DT	14-SEP-1993	(first entry)							
XX									
DE	[D-Ala132] rANVP (126-148)-NH2.								
XX									
KW	Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;								
KW	regulation; fluid volume; blood pressure.								
XX									
OS	Synthetic.								
XX									
FH	Key	Location/Qualifiers							
FT	Disulfide-bond	4..20							
FT	Misc-difference	7							
FT	Modified-site	/note= "D-form residue"							
FT		23							
FT		/note= "Amidated C-terminal"							
XX									
PN	US5212286-A.								
XX									
PD	18-MAY-1993.								
XX									
XX	05-JUN-1986;	86US-00870795.							
XX									
PR	19-APR-1984;	84US-00602117.							
PR	01-JUN-1984;	84US-00616488.							
PR	08-MAY-1985;	85US-00766030.							
XX									
PA	(SCIO-) SCIOS NOVA INC.								
XX									
PI	Lewicki JA, Scarborough RM;								
XX									
DR	WPI; 1993-175525/21.								
XX									
PT	New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator								
PT	in mammals.								
XX									
PS	Disclosure; Col 31; 45pp; English.								
XX									
CC	The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator								
CC	peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of								
CC	fluid volume and blood pressure in host organisms. These ANVP fragments								
CC	may be produced by solid-phase techniques. See also AAR36937-78. (Updated								
CC	on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct								
CC	PR field.)								
XX									
SQ	Sequence 23 AA;								
Query Match 82.4%; Score 56; DB 2; Length 23;									
Best Local Similarity 58.8%; Pred. No. 0.00046;									
Matches	10;	Conservative	0;	Mismatches	7;	Indels	0;	Gaps	0;
QY	1	CFGXXXDRIGXXSXGC	17						
DB	4	CFGARIDRIGAQSGLGC	20						
RESULT 28									
ID	AAR40622	standard; protein; 23 AA.							
XX									

AC	AAR40622;			
XX				
DT	25-MAR-2003	(revised)		
DT	14-SEP-1993	(first entry)		
XX				
DE	[Arg129] [D-Ala133]hANVP(130-151).			
XX				
KW	Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;			
KW	regulation; fluid volume; blood pressure.			
XX				
OS	Synthetic.			
XX				
FH	Key	Location/Qualifiers		
FT	Disulfide-bond	2.	.18	
FT	Misc-difference	5		
FT	/note= "D form residue"			
XX				
PN	US5212286-A.			
XX				
PD	18-MAY-1993.			
XX				
XX				
PF	05-JUN-1986;	86US-00870795.		
XX				
PR	19-APR-1984;	84US-00602117.		
PR	01-JUN-1984;	84US-00616488.		
PR	08-MAY-1985;	85US-00766030.		
XX				
PA	(SCIO-) SCIOS NOVA INC.			
XX				
PI	Lewicki JA, Scarborough RM;			
XX				
DR	WPI; 1993-175525/21.			
XX				
PT	New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator			
PT	in mammals.			
XX				
PS	Disclosure; Col 47; 45pp; English.			
XX				
CC	The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator			
CC	peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of			
CC	fluid volume and blood pressure in host organisms. These ANVP fragments			
CC	may be produced by solid-phase techniques. See also AAR36937-78. (Updated			
CC	on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct			
CC	PR field.)			
XX				
SQ	Sequence 23 AA;			
	Query Match	82.4%;	Score 56;	DB 2; Length 23;
	Best Local Similarity	58.8%;	Pred. No. 0.00046;	
	Matches 10;	Conservative 0;	Mismatches 7;	Indels 0; Gaps 0
QY	1	CFGXXXDRIGXXSXXGC 17		
Db	2	CFGARMDRIGAGSGLGC 18		
RESULT 29				
ID	AAR40625 standard; protein; 23 AA.			
XX				
AC	AAR40625;			
XX				
DT	25-MAR-2003	(revised)		
DT	14-SEP-1993	(first entry)		
XX				
DE	[Arg128] [D-Ala142]rANVP(129-150).			
XX				
KW	Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;			
KW	regulation; fluid volume; blood pressure.			
XX				
OS	Synthetic.			
XX				
FH	Key	Location/Qualifiers		

FT Disulfide-bond 2.18
FT Misc-difference 15 /note= "D form residue"
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 47; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 23 AA;

Query Match 82.4%; Score 56; DB 2; Length 23;
Best Local Similarity 58.8%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| | ||
Db 2 CFGGRMDRIGAQSLGC 18

RESULT 30
AAR40628
ID AAR40628 standard; protein; 23 AA.
XX
AC AAR40628;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg129] [D-Ala143] hANVP (130-151).
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Disulfide-bond 2.18
FT Misc-difference 15 /note= "D form residue"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.

XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 48; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 23 AA;

Query Match 82.4%; Score 56; DB 2; Length 23;
Best Local Similarity 58.8%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| | ||
Db 2 CFGGRMDRIGAQSLGC 18

RESULT 31

AAR40619
ID AAR40619 standard; protein; 23 AA.

XX
AC AAR40619;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [Arg129] [D-Ala132] rANVP (129-150).
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.

FH Key Location/Qualifiers
FH Disulfide-bond 2.18
FT Misc-difference 5 /note= "D form residue"
FT
XX
PN US5212286-A.

XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 47; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator

CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 23 AA;

Query Match 82.4%; Score 56; DB 2; Length 23;
Best Local Similarity 58.8%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||||| |
Db 2 CFGARIDRIGAGSGLGC 18

RESULT 32
AAR03303
ID AAR03303 standard; peptide; 24 AA.
XX
AC AAR03303;

DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 15-AUG-1990 (first entry)
XX
DE fANP-24 frog atrial natriuretic peptide.

XX
KM Atrial natriuretic peptide; fANP-24; diuretic; hypertensive.
XX
OS Rana catesbeiana.

FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
XX
PN JP02025500-A.

PD 26-JAN-1990.

PF 14-JUL-1988; 88JP-00173740.

PR 14-JUL-1988; 88JP-00173740.

XX
PA (MATS/) MATSUO T.

DR WPI; 1990-071805/10.

XX
PT New peptide with physiological activity - obtd. from heart of frog, has
PT diuretic and antihypertensive properties.

PS Claim 1; Fig 3; 8pp; Japanese.

XX
CC First three amino acids may be absent, see AAR03304. (Updated on 25-MAR-
CC 2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||||| |
Db 4 CFGSRIDRIGAGSGMGC 20

RESULT 33
AAR04818
ID AAR04818 standard; protein; 24 AA.
XX
AC AAR04818;

XX
DT 26-SEP-1990 (first entry)

XX
DE Peptide with Agonist and antagonist activity to ANP.

XX
KW ANP; agonist; antagonist; penicillamine.

XX
OS Synthetic.

FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
FT Modified-site 4

FT /label= Cys D-Cys penicillamine or D-penicillamine
FT /note= "AA 4 and 20 may not both be Cys."

FT Modified-site 20

FT /label= Cys D-Cys penicillamine or D-penicillamine
FT /note= "AA 4 and 20 may not both be Cys."

XX
PN JP02096594-A.

XX
PD 09-APR-1990.

PF 30-SEP-1988; 88JP-00246543.

PR 30-SEP-1988; 88JP-00246543.

XX
PA (SUNR) SUNTORY LTD.

XX
DR WPI; 1990-151858/20.

XX
PT New peptide(s) with agonist and antagonist activity to ANP - contg. at
PT least 15 amino-acid units and di:sulphide bridge.

XX
PS Claim 4; Page 930; 24pp; Japanese.

XX
CC Six N-terminal and five C-terminal acids may be shortened or absent

XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| ||||| |
Db 4 CFGSRIDRIGAGSGMGC 20

RESULT 34
AAR04813
ID AAR04813 standard; protein; 24 AA.
XX
AC AAR04813;

DT 26-SEP-1990 (first entry)

XX
DE Peptide antagonistic to ANP.

XX
KW Atrial natriuretc factor; antagonist.

XX
OS Synthetic.

FH Key Location/Qualifiers
FT Modified-site 4

FT /label= OTHER
FT /note= "CH2NHCOME, CH2CH2Q (where Q = 4-pyridyl or 2-
FT quinoilyl), CH2CONH2, CH2Ph, CH2COOH,SO3H,
FT CH3,CH2CONHC8H17 ORCH2CH2NH2"

FT Modified-site 20

FT /label= OTHER

FT /note= "CH2NHCOME, CH2CH2Q (where Q = 4-pyridyl or 2-
FT quinoilyl), CH2CONH2, CH2Ph, CH2COOH,SO3H,
FT CH3,CH2CONHC8H17 ORCH2CH2NH2"

XX JF02096595-A.
PN 09-APR-1990.
XX 30-SEP-1988; 88JP-00246544.
XX 30-SEP-1988; 88JP-00246544.
XX (SUNR) SUNTORY LTD.
XX WPI; 1990-151859/20.
XX New peptide - has antagonistic activity against ANP.
XX Claim 4; Page 3; 14pp; Japanese.
XX See also AAR04811-14
XX Sequence 24 AA;
SQ

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 35
AAR40453
ID AAR40453 standard; protein; 24 AA.
XX AAR40453;
AC 25-MAR-2003 (revised)
XX 14-SEP-1993 (first entry)
DT [D-Ala143]rANVP(127-150)-NH2.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
FT Misc-difference 17 /note= "D-form residue"
FT Modified-site 24 /note= "Amidated C-terminal"
XX
XX US5212286-A.
PN 18-MAY-1993.
XX
PD 05-JUN-1986; 86US-00870795.
XX
PF 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
XX (SCIO-) SCIOS NOVA INC.
XX
XX PI Lewicki JA, Scarborough RM;
XX WPI; 1993-175525/21.
XX
XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX
PS Disclosure; Col 33; 45pp; English.

XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
XX Sequence 24 AA;
SQ

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
Db 4 CFGGRMDRIGAQSALGC 20

RESULT 36
AAR40446
ID AAR40446 standard; protein; 24 AA.
XX AAR40446;
AC 25-MAR-2003 (revised)
XX 14-SEP-1993 (first entry)
DT [D-Ala142]rANVP(126-149).
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
FT Misc-difference 17 /note= "D-form residue"
FT
XX
XX US5212286-A.
PN 18-MAY-1993.
XX
PD 05-JUN-1986; 86US-00870795.
XX
PF 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
XX (SCIO-) SCIOS NOVA INC.
XX
XX PI Lewicki JA, Scarborough RM;
XX WPI; 1993-175525/21.
XX
PD New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX
PF Disclosure; Col 33; 45pp; English.
XX
XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
XX Sequence 24 AA;
SQ

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXGC 17
||| ||| |
Db 4 CFGGRIDRIGAQSALGC 20

RESULT 37
AAR40432
ID AAR40432 standard; protein; 24 AA.
XX
AC AAR40432;
XX

DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX

DE [D-Ala133]hANVP(127-150)-NH2.

XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KM regulation; fluid volume; blood pressure.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
FT Misc-difference 7

FT Modified-site 24 /note= "D-form residue"
FT /note= "Amidated C-terminal"

XX
PN US5212286-A.

XX
PD 18-MAY-1993.

PF 05-JUN-1986; 86US-00870795.

XX
PS 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX
PA (SCIO-) SCIOS NOVA INC.

XX
PI Lewicki JA, Scarborough RM;

XX
DR WPI; 1993-175525/21.

XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

XX
PS Disclosure; Col 32; 45pp; English.

XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXGC 17
||| ||| |
Db 4 CFGGRMDRIGAQSGLGC 20

RESULT 38
AAR40452
ID AAR40452 standard; protein; 24 AA.
XX
AC AAR40452;

XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [D-Ala143] rANVP(127-150).
XX

KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KM regulation; fluid volume; blood pressure.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
FT Misc-difference 17

FT /note= "D-form residue"

XX
PN US5212286-A.

XX
PD 18-MAY-1993.

PF 05-JUN-1986; 86US-00870795.

XX
PS 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX
PA (SCIO-) SCIOS NOVA INC.

XX
PI Lewicki JA, Scarborough RM;

XX
DR WPI; 1993-175525/21.

XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

XX
PS Disclosure; Col 33; 45pp; English.

XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXGC 17
||| ||| |
Db 4 CFGGRMDRIGAQSALGC 20

RESULT 39
AAR40431
ID AAR40431 standard; protein; 24 AA.
XX
AC AAR40431;

XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX

DE [D-Ala133]hANVP(127-150).

XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KM regulation; fluid volume; blood pressure.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .20

FT Misc-difference 7 /note= "D-form residue"
FT XX
PN US5212286-A.
XX PD 18-MAY-1993.
XX PF 05-JUN-1986; 86US-00870795.
XX PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX PA (SCIO-) SCIOS NOVA INC.
XX PI Lewicki JA, Scarborough RM;
XX WPI; 1993-175525/21.
DR
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 32; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
CC
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| | ||
Db 4 CFGARMDRIGAQSGLGC 20

RESULT 40
AAR40425
ID AAR40425 standard; protein; 24 AA.
XX
AC AAR40425;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [D-Ala132]rANVP(126-149).
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
FT Misc-difference 7 /note= "D-form residue"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX

PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 31; 45pp; English.
XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
CC
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| | ||
Db 4 CFGARMDRIGAQSGLGC 20

RESULT 41
AAR40426
ID AAR40426 standard; protein; 24 AA.
XX
AC AAR40426;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [D-Ala132]rANVP(126-149)-NH2.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
FT Misc-difference 7 /note= "D-form residue"
FT Modified-site 24 /note= "Amidated C-terminal"
FT
XX
PN US5212286-A.
XX
PD 18-MAY-1993.
XX
PF 05-JUN-1986; 86US-00870795.
XX
PR 19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
PA (SCIO-) SCIOS NOVA INC.
XX
PI Lewicki JA, Scarborough RM;
XX
DR WPI; 1993-175525/21.
XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
XX
PS Disclosure; Col 31; 45pp; English.
XX

CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)

XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXSXXGC 17
||| ||||| |
Db 4 CFGARIDRIGAQSGLGC 20

RESULT 42
AAR40447
ID AAR40447 standard; protein; 24 AA.
XX
AC AAR40447;

XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)

XX
DE [D-Ala142] rANVP(126-149)-NH2.

XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 4..20

FT Misc-difference 17

FT /note= "D-form residue"

FT Modified-site 24 /note= "Amidated C-terminal"

XX
PN US5212286-A.

XX
PD 18-MAY-1993.

XX
PF 05-JUN-1986; 86US-00870795.

XX
PR 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX
PA (SCIO-) SCIOS NOVA INC.

XX
PI Lewicki JA, Scarborough RM;

XX
DR WPI; 1993-175525/21.

XX
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.

XX
PS Disclosure; Col 33; 45pp; English.

XX
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)

XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXSXXGC 17
||| ||||| |
Db 4 CFGGRIDRIGAQSALGC 20

RESULT 43
AAW70091
ID AAW70091 standard; peptide; 24 AA.

XX
AC AAW70091;

XX
DT 28-OCT-1998 (first entry)

XX
DE Atrial natriuretic peptide (ANP) sequence.

XX
KW ANP; atrial natriuretic peptide; cardiac disease; cardiac hypertrophy;
KW chronic heart failure; ischemic cardiac disease; arrhythmia; cGMP;
KW pulmonary blood circulation; haemodynamic property.

XX
OS Unidentified.

XX
PN W09834636-A1.

XX
PD 13-AUG-1998.

XX
PF 05-FEB-1998; 98WO-JP000483.

XX
PR 05-FEB-1997; 97JP-00022594.

XX
PA (SUNR) SUNTORY LTD.

XX
PI Inomata N, Yamaki A, Furuya M, Hidaka T;

XX
DR WPI; 1998-446949/38.

XX
PT Drug composition comprises natriuretic peptide(s) - for safe treatment of
PT cardiac hypertrophy associated diseases and chronic heart failure.

XX
PS Example; Page 23; 35pp; Japanese.

XX
CC This represents an atrial natriuretic peptide (ANP) sequence. The
CC invention provides a composition for treating cardiac diseases associated
CC with cardiac hypertrophy. The composition comprises an active ingredient
CC capable of binding to the peptide receptor of GC-A and promoting
CC production of cGMP. The drug composition may be used clinically to treat
CC cardiac diseases caused by cardiac hypertrophy, including chronic heart
CC failure, ischaemic cardiac diseases and arrhythmia. The active substance
CC can bind to the natriuretic peptide receptor of GC-A and promote
CC production of cGMP, effectively preventing cardiac hypertrophy and
CC leading to improvement of the pulmonary blood circulation. The substance
CC does not affect haemodynamic properties, blood pressure, heart beat and
CC urine volume

XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXSXXGC 17
||| ||||| |
Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 44
AAB91295
ID AAB91295 standard; peptide; 24 AA.

XX
AC AAB91295;

XX
DT 22-JUN-2001 (first entry)

XX Atrial-natriuretic peptide (ANP) SEQ ID NO:471.
DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
XX
PS Disclosure; Page 353; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 4; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXGC 17
||| ||||| | ||
Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 45
AAB91292
ID AAB91292 standard; peptide; 24 AA.
XX
AC AAB91292;
XX
DT 22-JUN-2001 (first entry)
XX
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:468.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
OS Synthetic.
OS
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
XX
PS Disclosure; Page 352; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 4; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXGC 17
||| ||||| | ||
Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 46
AAE12435
ID AAE12435 standard; peptide; 24 AA.
XX
AC AAE12435;
XX
DT 03-JAN-2002 (first entry)
XX
DE Frog atrial natriuretic peptide (ANP) #2.
XX
KW Prophylaxis; ischaemic heart disease; myocardial infarction; frog;
KW ischaemia reperfusion injury; ischaemic heart disease; infarct region;
KW vasotropic; atrial natriuretic peptide; ANP.
XX
OS Rana sp.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .20
XX

PN US2001027181-A1.
XX
PD 04-OCT-2001.
XX
PF 03-JAN-2001; 2001US-00752724.
XX
PR 31-MAR-2000; 2000JP-00098134.
XX
PA (KITA/) KITAKAZE M.
XX
PI Kitakaze M;
XX
DR WPI; 2001-638528/73.
XX
PT Composition for the treatment or prophylaxis of ischemic heart disease
PT i.e. myocardial infarction, comprises a substance which can increase
PT intracellular cGMP production by acting on a natriuretic peptide
PT receptor.
XX
PS Disclosure; Page 4; 9pp; English.
XX
CC The invention relates to a pharmaceutical composition for the treatment
CC or prophylaxis of ischaemic heart disease, comprises a substance as an
CC active ingredient, which can increase intracellular cGMP production by
CC acting on a natriuretic peptide receptor and which has an effect of
CC reducing an infarct region. The composition is useful for suppressing
CC ischaemia reperfusion injury in the treatment of ischaemic heart disease,
CC preferably myocardial infarction. The present sequence is frog atrial
CC natriuretic peptide (ANP)
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 4; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXGC 17
||| |||| | ||
Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 47
ADV86892
ID ADV86892 standard; peptide; 24 AA.
XX
AC ADV86892;
XX
DT 10-MAR-2005 (first entry)
XX
DE Bovine ANP peptide fragment.
XX
KW Immunosuppressive; Anti-rheumatic; Anti-arthritis; Antidiabetic;
KW Anti-inflammatory; Anticancer; Gastrointestinal-Gen.; Neuroprotective;
KW Antiparasitic; Dermatological; Muscular-Gen.; Thyromimetic;
KW guanosine monophosphate; GMP; Guanylyl cyclase A-modulator;
KW atrial natriuretic peptide; ANP; immune disorder;
KW cerebral natriuretic peptide.
XX
OS Bos sp.
XX
PN WO2004110489-A1.
XX
PD 23-DEC-2004.
XX
PF 11-JUN-2004; 2004WO-JP008205.
XX
PR 13-JUN-2003; 2003JP-00169370.
XX
PA (SUNR) DAIICHI SUNTORY PHARMA CO LTD.
XX
PI Hori T;
XX
DR WPI; 2005-066084/07.

XX
PT Composition comprising natriuretic-peptide acting on guanylyl cyclase A
PT and enhancing cyclic guanosine monophosphate production, useful for
PT prevention/treatment of Th1-type immunological disease e.g., autoimmune
PT disease.
XX
PS Disclosure; SEQ ID NO 5; 32pp; Japanese.
XX
CC This sequence represents a fragment of an atrial natriuretic-peptide.
CC This peptide may be used in a pharmaceutical composition for prevention
CC or treatment of Th1-type immunological disease. The composition comprises
CC a substance capable of acting on guanylyl cyclase A, which is a
CC natriuretic-peptide receptor and enhancing cyclic guanosine monophosphate
CC production, as an active ingredient. The claimed substance may be used
CC for controlling Th1/Th2 balance in the immune system to induce Th2
CC deflection property. In the claimed composition, the guanylyl cyclase A
CC is natriuretic-peptide receptor. The substance is a natriuretic-peptide
CC which is an atrial or cerebral natriuretic-peptide. The atrial
CC natriuretic-peptide is preferably of human origin. The enhancement of
CC cyclic guanosine monophosphate (cGMP) production by atrial natriuretic-
CC peptide (ANP) was determined in vitro . RNA was synthesized from the
CC monocyte obtained from the peripheral blood of a healthy subject. The
CC dendritic cells were allowed to react with ANP and with cerebral
CC natriuretic peptide (CNP) (control) . The ANP raised cGMP in dendritic
CC cell at a higher concentration of 10-12 M than in monocytes. CNP did not
CC influence intracellular cGMP concentration in monocytes or dendritic
CC cells. The composition is useful for preventing or treating Th1-type
CC immunological disease chosen from graft-versus-host disease, autoimmune
CC disease, disease resulting from bone marrow transplant and immunological
CC disease resulting from transplant rejection. The autoimmune disease are
CC autoimmune hepatitis, rheumatoid arthritis, insulin-dependent diabetes
CC mellitus, ulcerative colitis, Crohns' disease, multiple sclerosis,
CC autoimmune myocarditis, psoriasis, scleroderma, myasthenia gravis,
CC multiple myocytis, dermatomyocytis, Hashimoto's disease, autoimmune
CC hypocytosis (erythroblastosis, hypoplastic anemia, etc.), Sjogrens 's
CC syndrome, angitis syndrome and systemic lupus erythematosus, preferably
CC Crohns' disease or multiple sclerosis. The claimed substance is useful
CC for treating Th1-type immunological disease, for manufacturing a
CC pharmaceutical composition for preventing or treating Th1-type
CC immunological disease, and for controlling Th1/Th2 balance in the immune
CC system. The claimed composition enables control of Th1/Th2 balance in an
CC immune system by using the substance which acts on guanyl cyclase A.
CC Note: This sequence is not given in the specification.
XX
SQ Sequence 24 AA;

Query Match 82.4%; Score 56; DB 9; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXGC 17
||| |||| | ||
Db 4 CFGSRIDRIGAQSGMGC 20

RESULT 48
AAR40424
ID AAR40424 standard; protein; 25 AA.
XX
AC AAR40424;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [D-Ala132] rANVP (126-150)-NH2.
XX
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT Disulfide-bond 4. .20

FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 25
 FT /note= "Amidated C-terminal"
 XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI; 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 31; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC
 XX
 SQ Sequence 25 AA;

Query Match 82.4%; Score 56; DB 2; Length 25;
 Best Local Similarity 58.8%; Pred. No. 0.0005;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCGXXDXDRIGXXSXGC 17
 ||| ||| ||| |||
 Db 4 CFCGARIDRIGAGSGLGC 20

RESULT 49
 AAR40587
 ID AAR40587 standard; protein; 25 AA.
 XX
 AC AAR40587;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE [Ala132]rANVP(126-150).
 XX
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 4. .20
 XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX

PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI; 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 44; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC
 XX
 SQ Sequence 25 AA;

Query Match 82.4%; Score 56; DB 2; Length 25;
 Best Local Similarity 58.8%; Pred. No. 0.0005;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCGXXDXDRIGXXSXGC 17
 ||| ||| ||| |||
 Db 4 CFCGARIDRIGAGSGLGC 20

RESULT 50
 AAR40451
 ID AAR40451 standard; protein; 25 AA.
 XX
 AC AAR40451;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE [D-Ala143]rANVP(127-151)-NH2.
 XX
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 4. .20
 FT Misc-difference 17
 FT /note= "D-form residue"
 FT Modified-site 25 /note= "Amidated C-terminal"
 XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI; 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 33; 45pp; English.
 XX

CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX

SQ Sequence 25 AA;

Query Match 82.4%; Score 56; DB 2; Length 25;
Best Local Similarity 58.8%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
Db 4 CFGGRMDRIGAQSALGC 20

Search completed: January 26, 2006, 14:43:41
Job time : 84 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 26, 2006, 14:39:17 ; Search time 17 Seconds
(without alignments)
96.217 Million cell updates/sec

Title: US-10-664-605-5
Perfect score: 68
Sequence: 1 CFGXXXDRIGXXSXXGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	82.4	30	2	S01657 atrial natriuretic
2	56	82.4	128	2	S14872 atrial natriuretic
3	56	82.4	145	1	JQ0947 atrial natriuretic
4	55	80.9	22	2	JT0581 natriuretic peptid
5	55	80.9	22	2	A35418 brain natriuretic
6	55	80.9	22	2	A36399 C-type natriuretic
7	55	80.9	27	2	JC1081 brain natriuretic
8	55	80.9	27	2	A33431 atrial natriuretic
9	55	80.9	36	2	S15821 ventricular natriu
10	55	80.9	38	2	S71381 lebetin 2 isoform
11	55	80.9	103	2	A41403 aldosterone secret
12	55	80.9	105	2	B36736 brain natriuretic
13	55	80.9	115	1	S15822 natriuretic peptid
14	55	80.9	118	2	B54119 C-type natriuretic
15	55	80.9	121	1	A30162 brain natriuretic
16	55	80.9	121	1	A49144 type-B natriuretic
17	55	80.9	121	2	I49548 brain natriuretic
18	55	80.9	126	1	A36155 natriuretic peptid
19	55	80.9	126	1	AMHUC natriuretic peptid
20	55	80.9	126	2	A55688 natriuretic peptid
21	55	80.9	126	2	S12988 brain natriuretic
22	55	80.9	129	1	A54119 C-type natriuretic
23	55	80.9	131	2	A33873 brain natriuretic
24	55	80.9	131	2	A33873 natriuretic peptid
25	55	80.9	135	1	A61244 alpha-atrial natri
26	55	80.9	140	1	S14320 atrial natriuretic
27	55	80.9	149	1	AWDG atrial natriuretic
28	55	80.9	150	1	S13107 atrial natriuretic
29	55	80.9	151	1	AMHU natriuretic peptid

30	55	80.9	152	1	AWBO atrial natriuretic
31	55	80.9	152	1	AMMS atrial natriuretic
32	55	80.9	152	1	AMRT atrial natriuretic
33	55	80.9	153	1	AMRB atrial natriuretic
34	55	80.9	153	1	S14873 natriuretic peptid
35	55	80.9	161	4	I55480 natriuretic peptid
36	50	73.5	134	1	AMHUB natriuretic peptid
37	48	70.6	38	2	A42974 natriuretic peptid
38	37	54.4	1067	2	T18196 pol protein - silk
39	36	52.9	541	2	T34850 probable acid-CoA
40	35	51.5	113	2	S66859 hypothetical prote
41	35	51.5	2110	2	B44110 mycocerosate synth
42	35	51.5	2111	2	A70668 mycocerosate synth
43	35	51.5	2116	2	C86926 probable mycoceros
44	35	51.5	2118	2	S72705 mycocerosate synth
45	34	50.0	327	2	AI1422 hypothetical prote
46	34	50.0	504	2	H97462 hypothetical prote
47	34	50.0	648	2	S50856 whn protein - rat
48	34	50.0	2108	2	H70819 probable polyketid
49	33	48.5	137	2	A97088 uncharacterized pr
50	33	48.5	419	2	T10652 hypothetical prote
51	33	48.5	472	1	WMADP6 early E1B 52K prot
52	33	48.5	475	1	WMADP6 early E1B 53K prot
53	32	47.1	66	2	T43057 spermiogenesis pro
54	32	47.1	315	2	T32059 hypothetical prote
55	32	47.1	347	2	T02669 hypothetical prote
56	32	47.1	411	2	A87390 transporter, proba
57	32	47.1	433	2	AG0831 alpha-ketoglutarat
58	32	47.1	437	2	H83175 probable MFS trans
59	32	47.1	446	2	A42661 citrate carrier pr
60	32	47.1	446	2	AD0509 citrate-sodium sym
61	32	47.1	446	2	B42661 citrate carrier pr
62	32	47.1	462	2	D83117 probable MFS trans
63	32	47.1	488	2	H90423 sugar transport pr
64	32	47.1	509	2	JH0501 zinc finger protei
65	32	47.1	519	2	T45764 hypothetical prote
66	32	47.1	566	2	S17477 hypothetical prote
67	32	47.1	1871	2	A87204 polyketide synthas
68	31	45.6	260	2	A83457 conserved hypothet
69	31	45.6	286	2	AG3276 protein eIFK/srIk
70	31	45.6	319	2	T36988 probable secreted
71	31	45.6	369	2	C97484 outer membrane pro
72	31	45.6	369	2	AC2702 outer membrane pro
73	31	45.6	387	2	F84392 hypothetical prote
74	31	45.6	400	2	C69757 transporter homolo
75	31	45.6	407	2	C64167 hypothetical prote
76	31	45.6	412	1	XNCHDC aspartate transami
77	31	45.6	432	2	A83616 dicarboxylic acid
78	31	45.6	450	2	F95360 probable transemb
79	31	45.6	454	2	AC0444 probable metabolit
80	31	45.6	454	2	AD0556 hypothetical major
81	31	45.6	456	1	C64772 probable transport
82	31	45.6	456	2	E85539 probable transport
83	31	45.6	456	2	A90689 probable transport
84	31	45.6	462	2	AI0384 phosphomannomutase
85	31	45.6	462	2	F64163 3-isopropylmalate
86	31	45.6	469	2	T30983 hypothetical prote
87	31	45.6	482	2	TF1827 alpha, alpha-trehal
88	31	45.6	495	2	A96792 probable phosphate
89	31	45.6	532	2	A96792 ferrichrome-iron r
90	31	45.6	872	2	AC2134 probable polyketid
91	31	45.6	1582	2	E70876 hypothetical prote
92	31	45.6	1890	2	T04556 calcium channel pr
93	31	45.6	2220	2	A45290 hypothetical prote
94	30	44.1	137	2	B83475 hypothetical prote
95	30	44.1	172	2	E72472 matrix protein M1
96	30	44.1	211	2	G70981 conserved hypothet
97	30	44.1	252	1	MFIV1F hypothetical prote
98	30	44.1	258	2	H96013 hypothetical prote
99	30	44.1	264	2	T37551 hypothetical prote
100	30	44.1	270	2	D71301 hypothetical prote
101	30	44.1	307	2	AF2402 cell adhesion glyc
102	30	44.1	320	2	A53119

103	30	44.1	353	2	S37873	hypothetical prote
104	30	44.1	354	2	S60242	cinamyl-alcohol d
105	30	44.1	366	2	B86341	hypothetical prote
106	30	44.1	397	2	S27600	N-acetylglutamate
107	30	44.1	398	1	D64464	hypothetical prote
108	30	44.1	406	2	C84940	3-oxacyl-lacyl-ca
109	30	44.1	409	2	A84602	hypothetical prote
110	30	44.1	414	2	H95999	probable N-carbam
111	30	44.1	427	2	G85719	probable transpor
112	30	44.1	427	2	B64909	probable membrane
113	30	44.1	427	2	H90897	probable transpor
114	30	44.1	429	2	T08562	hypothetical prote
115	30	44.1	459	2	AE0679	probable membrane
116	30	44.1	469	2	E83195	phosphate transp
117	30	44.1	471	2	H90502	phosphate transp
118	30	44.1	495	2	A95984	probable xanthine
119	30	44.1	514	2	B96585	hypothetical prote
120	30	44.1	521	2	S67491	phosphate transpor
121	30	44.1	566	2	A72329	general secretion
122	30	44.1	645	2	AE2655	conserved hypothet
123	30	44.1	672	2	A97437	hypothetical 71.3K
124	30	44.1	683	2	C71322	probable translati
125	30	44.1	830	2	E83031	conserved hypothet
126	30	44.1	861	2	B49847	nitrate reductase
127	30	44.1	863	2	D88216	protein B0495.7 [i
128	30	44.1	1140	1	I38908	UV-damaged DNA-bin
129	30	44.1	1140	1	S38777	UV-damaged DNA-bin
130	30	44.1	1140	2	JC7152	UV-damaged DNA-bin
131	30	44.1	1331	1	XORTDH	xanthine dehydroge
132	30	44.1	1335	1	XOMSDH	xanthine dehydroge
133	30	44.1	2514	2	T37320	ataxia telangiecta
134	30	44.1	2619	2	T24588	hypothetical prote
135	29	42.6	121	2	A49590	Ig heavy chain V r
136	29	42.6	137	2	G97352	uncharacterized co
137	29	42.6	145	2	A81992	hypothetical prote
138	29	42.6	145	2	E81222	hypothetical prote
139	29	42.6	265	2	D83577	conserved hypothet
140	29	42.6	344	2	C82611	hypothetical prote
141	29	42.6	349	2	H75468	conserved hypothet
142	29	42.6	357	2	T29856	probable aspartate
143	29	42.6	362	2	A70547	probable menE - My
144	29	42.6	368	2	E87191	o-succinylbenzoic
145	29	42.6	371	2	B90267	transport protein,
146	29	42.6	378	2	T25885	hypothetical prote
147	29	42.6	399	2	D83535	aromatic amino aci
148	29	42.6	399	2	T23470	hypothetical prote
149	29	42.6	414	2	D82487	multidrug resistanc
150	29	42.6	419	1	DEECNB	glycerol-3-phospha
151	29	42.6	419	2	A85864	hypothetical prote
152	29	42.6	419	2	G91019	hypothetical prote
153	29	42.6	422	2	C70518	probable nanf prot
154	29	42.6	431	2	D83160	nitrite extrusion
155	29	42.6	434	2	G97610	hypothetical metab
156	29	42.6	434	2	AC2833	hypothetical prote
157	29	42.6	438	2	G64962	shikimate transpor
158	29	42.6	438	2	B90976	shikimate transpor
159	29	42.6	438	2	H85822	probable transpor
160	29	42.6	440	2	AD0986	hypothetical metab
161	29	42.6	440	2	S47743	probable sugar tra
162	29	42.6	440	2	D86025	probable transpor
163	29	42.6	440	2	C91179	probable transpor
164	29	42.6	455	2	AD1329	UDP-N-acetylmuram
165	29	42.6	455	2	AD1700	UDP-N-acetylmuram
166	29	42.6	481	2	G82125	Na+/H+ antiporter
167	29	42.6	498	2	T20646	hypothetical prote
168	29	42.6	504	2	AG1847	anthranilate synth
169	29	42.6	508	2	G71654	phosphomannomutase
170	29	42.6	536	2	T19488	hypothetical prote
171	29	42.6	578	2	D69165	hypothetical prote
172	29	42.6	627	2	B48442	membrane transport
173	29	42.6	645	2	F70825	probable PPE prote
174	29	42.6	654	2	T34613	NADH2 dehydrogenas
175	29	42.6	671	2	S61693	probable membrane
176	177	42.6	737	2	T46101	ABC transporter-li
177	29	42.6	819	2	C84615	hypothetical prote
178	29	42.6	867	2	T02579	hypothetical prote
179	29	42.6	1517	1	F65112	glutamate synthase
180	29	42.6	1517	2	F85985	glutamate synthase
181	29	42.6	1517	2	C91140	glutamate synthase
182	29	42.6	1588	2	T38660	probable transcrip
183	29	42.6	1701	2	T43213	ENBPI protein - ba
184	29	42.6	2126	2	E70522	probable polyketid
185	28.5	41.9	426	2	C84202	hypothetical prote
186	28	41.2	75	2	AC3445	H+-transporting tw
187	28	41.2	83	2	T35495	hypothetical prote
188	28	41.2	83	2	A45466	hypocine/tyrosine-r
189	28	41.2	144	2	T44915	superoxide dismuta
190	28	41.2	152	2	B97865	proline/betaine tr
191	28	41.2	180	2	B95966	hypothetical prote
192	28	41.2	189	2	S04670	hypothetical prote
193	28	41.2	197	2	AE2808	succinoglycan bios
194	28	41.2	224	2	D70665	probable urease ac
195	28	41.2	224	2	C97587	succinoglycan bios
196	28	41.2	231	2	H86463	F12G12.17 protein
197	28	41.2	234	2	D87629	transcription regu
198	28	41.2	235	2	H97197	uncharacterized pr
199	28	41.2	241	2	T31573	hypothetical prote
200	28	41.2	258	2	C64108	hypothetical prote
201	28	41.2	286	2	A69002	2-oxoglutarate syn
202	28	41.2	291	2	AC1305	hypothetical prote
203	28	41.2	291	2	AC1674	hypothetical prote
204	28	41.2	291	2	H84811	branched-chain aml
205	28	41.2	298	2	F81303	hypothetical prote
206	28	41.2	333	2	B42476	probable glycosylt
207	28	41.2	333	2	AC0766	Wnt-7b protein - m
208	28	41.2	349	2	H36470	phenylalanyl-cRNA
209	28	41.2	357	2	H87378	hypocyclomycin resis
210	28	41.2	397	2	AC2110	bicyclomycin resis
211	28	41.2	402	2	B75639	probable multidrug
212	28	41.2	412	2	S13035	aspartate transami
213	28	41.2	412	2	S29028	aspartate transami
214	28	41.2	413	2	UT0439	aspartate transami
215	28	41.2	413	2	S29027	aspartate transami
216	28	41.2	413	2	S01076	aspartate transami
217	28	41.2	413	2	D71112	hypothetical prote
218	28	41.2	415	2	D71647	proline/betaine tr
219	28	41.2	418	2	T39279	probable homocitrat
220	28	41.2	419	2	A81258	alpha-ketoglutarat
221	28	41.2	419	2	JQ1201	CmlA protein - Pse
222	28	41.2	419	2	A47033	chloramphenicol re
223	28	41.2	425	2	F70608	hypothetical prote
224	28	41.2	428	2	S58735	homocitrate syntha
225	28	41.2	431	2	B96006	probable metabolit
226	28	41.2	431	2	D81282	probable efflux pr
227	28	41.2	431	2	H90495	metabolite transpo
228	28	41.2	433	2	B98095	type III secretion
229	28	41.2	439	2	F85940	homocitrate syntha
230	28	41.2	440	1	S67674	probable Mtba prot
231	28	41.2	440	2	BF3321	alpha-ketoglutarat
232	28	41.2	457	2	G89825	hypothetical prote
233	28	41.2	466	2	T34748	transmembrane tran
234	28	41.2	472	2	F82639	resistance protein
235	28	41.2	472	2	T34748	hypothetical prote
236	28	41.2	475	2	T33985	hypothetical prote
237	28	41.2	478	2	S63659	NADH2 dehydrogenas
238	28	41.2	482	2	F95050	glutamyl-tRNA(Gln)
239	28	41.2	488	2	B97921	glu-tRNAAGln amidot
240	28	41.2	488	2	F71568	glutamyl-tRNA(Gln)
241	28	41.2	491	2	F71568	lysyl-tRNA synthet
242	28	41.2	491	2	H71253	probable glu-tRNA
243	28	41.2	506	2	E87233	probable secreted
244	28	41.2	519	2	A29600	alkaline phosphata
245	28	41.2	524	2	S66467	alkaline phosphata
246	28	41.2	524	2	S66467	alkaline phosphata
247	28	41.2	524	2	S66467	alkaline phosphata
248	28	41.2	524	2	S66467	alkaline phosphata

249	28	41.2	528	2	T30132	hypothetical prote	322	27	39.7	303	2	B96909	probable permease
250	28	41.2	556	2	G88941	protein R13D11.8 l	323	27	39.7	304	2	S67148	hypothetical prote
251	28	41.2	609	2	T45497	transposition prot	324	27	39.7	307	2	A71807	hypothetical prote
252	28	41.2	624	1	RDYCS7	sulfite reductase	325	27	39.7	307	2	JC5036	hypothetical prote
253	28	41.2	624	2	T49366	myocyte-specific e	326	27	39.7	307	2	E71206	hypothetical prote
254	28	41.2	650	2	A11974	ferredoxin-sulfite	327	27	39.7	311	2	T32860	hypothetical prote
255	28	41.2	664	2	D82056	ABC transporter, A	328	27	39.7	326	2	T51060	hypothetical prote
256	28	41.2	687	2	JQ1044	arylphorin precurs	329	27	39.7	326	2	A33755	hypothetical prote
257	28	41.2	691	2	F91251	probable tape meas	330	27	39.7	333	2	G81132	myb-induced myelo
258	28	41.2	717	2	T34514	hypothetical prote	331	27	39.7	333	2	H81188	NifR3/SM1 family
259	28	41.2	747	2	F69332	heterodisulfide re	332	27	39.7	337	2	S60577	hypothetical prote
260	28	41.2	757	2	F83516	hypothetical prote	333	27	39.7	338	2	B82432	porphobilinogen sy
261	28	41.2	783	2	E96652	protein F23M19.11	334	27	39.7	339	2	B86577	hypothetical prote
262	28	41.2	787	2	S35701	translation elonga	335	27	39.7	339	2	C72048	hypothetical prote
263	28	41.2	818	2	S62790	ismatch DNA recog	336	27	39.7	341	2	T31826	tptr repeats-ct683
264	28	41.2	831	2	T15108	hypothetical prote	337	27	39.7	347	2	G75283	hypothetical prote
265	28	41.2	870	2	B40121	GTPase-activating	338	27	39.7	350	2	A82798	asparaginase (EC 3
266	28	41.2	880	2	S51473	probable membrane	339	27	39.7	352	2	AB2248	hypothetical prote
267	28	41.2	928	2	S40745	hypothetical prote	340	27	39.7	356	2	H90289	N-acetyl-glutamate
268	28	41.2	975	2	C81728	metalloproteinase,	341	27	39.7	363	2	T39527	permease, sugar tr
269	28	41.2	996	1	S42208	NAD ADP-ribosyltra	342	27	39.7	374	2	F90361	hypothetical prote
270	28	41.2	1010	2	G88554	protein F54C8.3 li	343	27	39.7	375	1	A48257	transport membrane
271	28	41.2	1038	2	JT0663	ras GTPase-activat	344	27	39.7	375	1	I60970	alcohol dehydrogen
272	28	41.2	1044	2	S01966	GTPase-activating	345	27	39.7	375	1	I60973	alcohol dehydrogen
273	28	41.2	1047	2	A40121	GTPase-activating	346	27	39.7	376	2	S40470	mitogen-activated
274	28	41.2	1126	1	WMFM12	125K protein - alf	347	27	39.7	387	2	B90862	probable membrane
275	28	41.2	1148	2	T09073	splicing factor 2 -	348	27	39.7	397	2	F70001	multidrug resistan
276	28	41.2	1233	2	T04251	P-glycoprotein 2 -	349	27	39.7	400	2	C82503	hypothetical prote
277	28	41.2	1486	2	A10906	glutamate synthase	350	27	39.7	412	2	I39554	phosphoglycerate k
278	28	41.2	1489	2	A82524	glutamate synthase	351	27	39.7	413	2	I39551	phosphoglycerate k
279	28	41.2	1496	2	B81416	glutamate synthase	352	27	39.7	423	2	S74046	probable sugar tra
280	28	41.2	1538	2	AF0432	hypothetical prote	353	27	39.7	425	2	S56504	hypothetical 46.6K
281	28	41.2	2480	2	D84904	hypothetical prote	354	27	39.7	426	2	C90425	metabolite transpo
282	28	41.2	3164	1	MMBEH6	U36 protein - hum	355	27	39.7	426	2	AB3582	transporter, mfs s
283	27.5	40.4	367	2	T39574	probable uracil ki	356	27	39.7	427	2	B90371	metabolite transpo
284	27.5	40.4	434	2	T01013	hypothetical prote	357	27	39.7	427	2	G69067	N-ethylmeline ch
285	27.5	40.4	2437	2	S42612	transmembrane proc	358	27	39.7	431	2	A70588	probable mbtg prot
286	27	39.7	35	2	F82051	hypothetical prote	359	27	39.7	438	2	A64147	hypothetical prote
287	27	39.7	80	2	E83102	conserved hypothet	360	27	39.7	439	2	D86297	hypothetical prote
288	27	39.7	103	2	AG0237	probable cytochrom	361	27	39.7	443	2	H85485	probable transport
289	27	39.7	104	2	T47010	hypothetical prote	362	27	39.7	443	2	H90634	probable transport
290	27	39.7	128	2	I51603	gene Xcat-2 protei	363	27	39.7	443	2	E64725	yaau protein - Esc
291	27	39.7	133	2	S10038	hypothetical prote	364	27	39.7	446	2	B90463	proline/betaine tr
292	27	39.7	147	2	AH1021	conserved hypothet	365	27	39.7	448	1	A29830	benzene 1,2-dioxyg
293	27	39.7	152	2	H97405	hypothetical prote	366	27	39.7	448	2	H70947	hypothetical prote
294	27	39.7	163	2	S40924	hypothetical prote	367	27	39.7	454	2	F75580	probable sugar tra
295	27	39.7	178	2	D69467	probable orotate p	368	27	39.7	460	2	T35916	conserved hypothet
296	27	39.7	180	2	S18119	male protein homol	369	27	39.7	466	2	T07404	probable glucosylt
297	27	39.7	187	2	E72390	orotate phosphorib	370	27	39.7	470	2	S78440	phosphoglucomutase
298	27	39.7	192	2	B82232	thymidine kinase (371	27	39.7	473	2	H86240	hypothetical prote
299	27	39.7	196	2	D70470	conserved hypothet	372	27	39.7	475	2	A86811	beta-glucosidase (
300	27	39.7	196	2	AD0265	thymidine kinase (373	27	39.7	477	2	S50738	OR1 protein - yea
301	27	39.7	206	2	G82893	urease complex com	374	27	39.7	478	2	A72721	probable Glycerol
302	27	39.7	223	2	B96506	hypothetical prote	375	27	39.7	484	2	E82248	fatty oxidation co
303	27	39.7	226	2	C82124	oxidoreductase, sh	376	27	39.7	484	2	B64481	hypothetical prote
304	27	39.7	230	2	AD0894	conserved hypothet	377	27	39.7	485	2	F97228	glu-tRNAGln amidot
305	27	39.7	239	2	H72667	hypothetical prote	378	27	39.7	486	2	S30959	gene 14 protein -
306	27	39.7	239	2	H85756	partial probable m	379	27	39.7	496	2	T19776	hypothetical prote
307	27	39.7	259	2	C36819	C11 protein - rabb	380	27	39.7	498	2	B86436	protein F17F8.1 (i
308	27	39.7	262	2	T47607	hypothetical prote	381	27	39.7	500	2	T49388	related to ascus d
309	27	39.7	263	2	T50596	probable oxidoredu	382	27	39.7	501	2	G83848	cobyrlic acid synth
310	27	39.7	272	2	T08762	hypothetical prote	383	27	39.7	501	2	JC7877	toxin-60A - Okinaw
311	27	39.7	272	2	T14755	hypothetical prote	384	27	39.7	502	2	T00483	hypothetical prote
312	27	39.7	272	2	D87436	2-keto-4-pentenat	385	27	39.7	504	2	A83901	hypothetical prote
313	27	39.7	273	2	A84356	ATP-binding protei	386	27	39.7	505	2	AB3134	chlorohydrolyase li
314	27	39.7	282	2	H81358	probable signal pe	387	27	39.7	505	2	B98154	hypothetical prote
315	27	39.7	283	2	T46514	pathway-specific t	388	27	39.7	509	2	D84339	l-aspartate oxidas
316	27	39.7	283	2	D86143	hypothetical prote	389	27	39.7	510	2	T07119	cytochrome P450 CP
317	27	39.7	284	2	B64694	conserved hypothet	390	27	39.7	516	2	E86062	probable 2-compone
318	27	39.7	284	2	T34275	hypothetical prote	391	27	39.7	516	2	D91216	hypothetical 56.2K
319	27	39.7	292	2	G71701	succinate-CoA liga	392	27	39.7	517	2	JQ0872	uroporphyrinogen I
320	27	39.7	293	2	A12775	conserved hypothet	393	27	39.7	532	2	AC2237	hypothetical prote
321	27	39.7	293	2	G97555	hypothetical prote	394	27	39.7	532	2	H85035	hypothetical prote

395	27	39.7	537	1	YRHUB6	tyrosinase-related
396	27	39.7	551	2	C71606	ATP synthase alpha
397	27	39.7	558	2	B87098	conserved hypothe
398	27	39.7	558	2	G70879	hypothetical prote
399	27	39.7	575	2	T24681	hypothetical prote
400	27	39.7	576	2	C88950	protein R0985.11 f
401	27	39.7	585	2	I46686	complement compo
402	27	39.7	586	1	S47452	probable serine/ch
403	27	39.7	588	2	S40925	hypothetical prote
404	27	39.7	607	2	T39823	hypothetical prote
405	27	39.7	614	2	A12882	MFS permease [suga
406	27	39.7	632	2	AE3560	proline/betaine tr
407	27	39.7	656	2	B84547	hypothetical prote
408	27	39.7	657	2	G97658	hypothetical prote
409	27	39.7	699	2	F97721	elongation factor
410	27	39.7	699	2	B71723	translation elonga
411	27	39.7	701	2	S31150	translation elonga
412	27	39.7	701	2	H87143	elongation factor
413	27	39.7	701	2	E70827	probable fusa prot
414	27	39.7	707	2	JC7763	neuronal leucine-r
415	27	39.7	726	2	T33995	hypothetical prote
416	27	39.7	729	2	C69038	transcriptio
417	27	39.7	730	1	S24124	trimethylamine regu
418	27	39.7	773	2	T27382	hypothetical prote
419	27	39.7	786	2	S44837	K02D10.1 protein -
420	27	39.7	797	2	T05247	methionine-tRNA 1i
421	27	39.7	811	2	T04638	hypothetical prote
422	27	39.7	882	2	AF3036	nitrate reductase
423	27	39.7	885	2	G95980	probable nitrate r
424	27	39.7	903	2	E98249	nitrate reductase
425	27	39.7	915	2	B48225	probable proprotet
426	27	39.7	927	2	F82818	conserved hypothe
427	27	39.7	949	2	T16812	hypothetical prote
428	27	39.7	960	2	T07680	VPS41 protein homo
429	27	39.7	1063	2	T38420	probable DNA helic
430	27	39.7	1088	2	B85068	UV-damaged DNA bin
431	27	39.7	1102	2	T04941	UV-damaged DNA-bin
432	27	39.7	1115	2	T09433	integrin alpha cha
433	27	39.7	1115	2	T09403	integrin alpha cha
434	27	39.7	1139	2	T33275	hypothetical prote
435	27	39.7	1217	2	S52714	sericinB - silkwo
436	27	39.7	1260	1	TVRTNU	protein-tyrosine k
437	27	39.7	1319	2	S75705	hypothetical prote
438	27	39.7	1534	2	T30295	P-glycoprotein - T
439	27	39.7	1557	2	T28811	hypothetical prote
440	27	39.7	1603	2	T24098	hypothetical prote
441	27	39.7	1927	2	S01168	beta-glycosidase c
442	27	39.7	1928	2	JS0610	beta-galactosidase
443	27	39.7	2482	2	I48922	cation-independent
444	27	39.7	2483	1	A49617	insulin-like growt
445	27	39.7	2499	1	A30788	mannose 6-phosphat
446	27	39.7	2664	2	T28626	variant-specific s
447	27	39.7	3078	2	T28432	proline/betaine tr
448	26.5	39.0	435	2	B97846	glucagon receptor
449	26.5	39.0	485	2	JC4363	glucagon receptor
450	26.5	39.0	485	2	JQ1957	glutamine-tRNA lig
451	26.5	39.0	794	2	T09643	glutamine-tRNA lig
452	26.5	39.0	1680	2	A43434	turin (EC 3.4.21.7
453	26	38.2	66	2	G81163	bacterioferritin-a
454	26	38.2	70	1	XISR1A	insect toxin 1 - S
455	26	38.2	88	2	G34444	insect toxin 2 pre
456	26	38.2	101	2	AH2121	hypothetical prote
457	26	38.2	105	2	G72606	hypothetical prote
458	26	38.2	114	2	AE2761	hypothetical prote
459	26	38.2	133	2	C24925	lactose permease -
460	26	38.2	133	2	JH0270	chondromodulin II
461	26	38.2	140	2	A84284	hypothetical prote
462	26	38.2	144	2	D90089	60s ribosomal prot
463	26	38.2	152	1	G25973	pertussis toxin ch
464	26	38.2	157	2	T20794	hypothetical prote
465	26	38.2	167	2	C97542	hypothetical prote
466	26	38.2	169	2	AB2233	hypothetical prote
467	26	38.2	173	2	AB3450	invasion protein b
468	26	38.2	175	2	AG1984	hypothetical prote
469	26	38.2	178	2	H84253	chemotaxis protein
470	26	38.2	181	2	C97709	hypothetical prote
471	26	38.2	181	2	A71713	cdp-diacylglycerol
472	26	38.2	189	2	T23747	hypothetical prote
473	26	38.2	191	2	G83161	probable DNA inver
474	26	38.2	197	2	JC2320	hypothetical 22k p
475	26	38.2	199	2	B82315	hypothetical prote
476	26	38.2	200	2	F83008	hypothetical prote
477	26	38.2	216	2	J50245	Ig lambda chain NI
478	26	38.2	221	2	F81295	cytochrome-c oxida
479	26	38.2	221	2	T46918	hypothetical prote
480	26	38.2	232	1	A64538	cytochrome-c oxida
481	26	38.2	232	2	H71969	cytochrome oxidase
482	26	38.2	236	2	C35620	coenzyme F420 hydr
483	26	38.2	246	2	F70858	hypothetical prote
484	26	38.2	247	2	T27778	hypothetical prote
485	26	38.2	252	2	F70091	hypothetical prote
486	26	38.2	255	2	I38426	lymphocyte activat
487	26	38.2	255	2	E82363	conserved hypothe
488	26	38.2	258	2	A33953	enterotoxin D prec
489	26	38.2	259	2	T04850	hypothetical prote
490	26	38.2	261	2	B97589	1-2,3-butanediol d
491	26	38.2	261	2	AG2810	short chain dehydr
492	26	38.2	261	2	A12582	conserved hypothe
493	26	38.2	261	2	G97362	ATP synthase chain
494	26	38.2	268	2	AG0334	conserved hypothe
495	26	38.2	271	2	AD0250	conserved hypothe
496	26	38.2	276	2	C72458	hypothetical prote
497	26	38.2	277	2	JQ0927	3A protein - tomat
498	26	38.2	284	2	S17820	protoporphyrin IX
499	26	38.2	284	2	S76536	hypothetical prote
500	26	38.2	288	2	E83946	pyruvate synthase
501	26	38.2	294	2	C87449	phenylalanine-4-hy
502	26	38.2	296	2	A53372	lysR-type regulato
503	26	38.2	298	2	A49630	ubiquitin conjugat
504	26	38.2	299	2	H87567	hypothetical prote
505	26	38.2	300	2	F84365	probable isopenten
506	26	38.2	301	2	A83017	probable transcrip
507	26	38.2	303	1	P3BVA0	3A protein - brome
508	26	38.2	303	2	G84460	hypothetical prote
509	26	38.2	307	2	AF3487	diene lactone hydro
510	26	38.2	309	2	B64531	probable lacyl-car
511	26	38.2	309	2	F71976	probable lacyl-car
512	26	38.2	311	2	A81179	protein-export mem
513	26	38.2	312	2	E69753	efflux system homo
514	26	38.2	325	2	E96620	protein T30E16.27
515	26	38.2	327	2	H86829	ribose operon repr
516	26	38.2	327	2	G33282	DNA-binding protei
517	26	38.2	330	2	S60211	fomB protein - Str
518	26	38.2	333	2	A75365	conserved hypothe
519	26	38.2	335	2	S37304	spal protein - Sal
520	26	38.2	339	2	D87225	conserved membrane
521	26	38.2	341	2	JC1201	carboxymethylcellu
522	26	38.2	341	2	A70598	hypothetical prote
523	26	38.2	345	2	T14707	DNA ligase homolog
524	26	38.2	348	1	A69194	2-oxoacid-ferredox
525	26	38.2	352	2	C84603	probable pectinest
526	26	38.2	353	2	T04780	hypothetical prote
527	26	38.2	354	1	VGBBE7	glycoprotein D pre
528	26	38.2	354	2	D70808	probable regulator
529	26	38.2	360	2	E86690	hypothetical prote
530	26	38.2	362	2	G87470	Hyd family secret
531	26	38.2	362	2	C82070	conserved hypothe
532	26	38.2	364	2	H71440	hypothetical prote
533	26	38.2	364	2	E81702	phospholipase D fa
534	26	38.2	365	2	T15010	hypothetical prote
535	26	38.2	366	2	S46305	dihydrodipicolinat
536	26	38.2	376	2	S63613	probable ATP-bindi
537	26	38.2	376	2	T46096	hypothetical prote
538	26	38.2	378	2	S61992	SLG1 protein - Yea
539	26	38.2	380	2	T23546	hypothetical prote
540	26	38.2	382	2	S36476	E2 protein - human

541	26	38.2	382	2	T09632	YgaP protein - Lac	614	26	38.2	481	2	G82926	hypothetical prote
542	26	38.2	385	2	T26487	hypothetical prote	615	26	38.2	483	2	S40128	fascin - African c
543	26	38.2	388	2	T46229	hypothetical prote	616	26	38.2	484	2	T26190	hypothetical prote
544	26	38.2	389	2	AD1918	alcohol dehydrogen	617	26	38.2	484	2	T34504	hypothetical prote
545	26	38.2	391	2	H85063	hypothetical prote	618	26	38.2	484	2	S61870	hypothetical prote
546	26	38.2	393	2	G75503	maltose ABC transp	619	26	38.2	499	2	S39886	virr protein - Str
547	26	38.2	394	2	AG0962	multidrug resistan	620	26	38.2	500	2	B81250	probable site-spec
548	26	38.2	394	2	D90105	putative SAR DNA-b	621	26	38.2	503	2	B81690	probable sodium-tr
549	26	38.2	396	1	B65169	multidrug resistan	622	26	38.2	503	2	C71535	probable NADH (ubi
550	26	38.2	396	2	H86051	2-module integral	623	26	38.2	508	2	S74537	anthranilate synth
551	26	38.2	396	2	F91205	2-module integral	624	26	38.2	516	2	H82973	choline transporte
552	26	38.2	396	2	C87379	multidrug resistan	625	26	38.2	517	2	T03445	glucose-1-phosphat
553	26	38.2	401	2	B69501	sugar transporter	626	26	38.2	518	2	T45765	hypothetical prote
554	26	38.2	403	2	C83422	nitrate transporter	627	26	38.2	528	2	S35272	dihydrofolate redu
555	26	38.2	404	2	AC2159	hypothetical prote	628	26	38.2	530	2	A42730	trans-acting posit
556	26	38.2	406	2	G64362	2-isopropylmalate	629	26	38.2	533	2	T07894	probable inorganic
557	26	38.2	408	2	AF1599	aluminum resistanc	630	26	38.2	534	2	C84811	phosphate transpor
558	26	38.2	410	2	AB3546	aminobutyraldehyde	631	26	38.2	535	2	T47629	phosphate transpor
559	26	38.2	415	2	T44436	3-oxoacyl-lacyl-ca	632	26	38.2	535	2	H75369	conserved hypothet
560	26	38.2	415	2	D85061	probable adenosine	633	26	38.2	537	2	T07892	probable inorganic
561	26	38.2	416	2	JT0487	lactose permease -	634	26	38.2	537	2	S50344	aspergillopepsin h
562	26	38.2	416	2	JC2544	lactose carrier pr	635	26	38.2	539	2	JH0263	carboxy-terminal p
563	26	38.2	417	1	GREC	lactose permease -	636	26	38.2	540	2	T44683	precorrin methylas
564	26	38.2	417	2	H85528	galactoside permea	637	26	38.2	540	2	A95264	probable ABC trans
565	26	38.2	417	2	D90678	galactoside permea	638	26	38.2	540	2	AH3032	hypothetical prote
566	26	38.2	418	2	F83986	transporter BH2694	639	26	38.2	541	2	B87532	transporter, proba
567	26	38.2	418	2	C97713	proline/betaine tr	640	26	38.2	541	2	I41124	acyl CoA dehydroge
568	26	38.2	418	2	E71716	glycerol-3-phospha	641	26	38.2	542	2	JQ1005	glucose-1-phosphat
569	26	38.2	419	2	AC0792	hypothetical prote	642	26	38.2	542	2	T01124	probable phosphate
570	26	38.2	421	2	E71363	conserved hypothet	643	26	38.2	542	2	B87373	ABC transporter, A
571	26	38.2	425	2	F72315	conserved hypothet	644	26	38.2	543	2	T39345	cytochrome ccc3 pre
572	26	38.2	426	2	E95854	dihydroliipoamide S	645	26	38.2	545	1	A39193	3-dehydroquinatate d
573	26	38.2	428	2	AH3536	citrate transporte	646	26	38.2	545	2	T06264	probable acyl coen
574	26	38.2	429	2	F82961	Spa47 protein - Sh	647	26	38.2	546	2	C91274	probable acyl coen
575	26	38.2	430	2	C42284	citrate utilizatio	648	26	38.2	546	2	C86115	major facilitator
576	26	38.2	431	1	ZTEC3	citrate utilizatio	649	26	38.2	550	2	A87252	ATP-binding protei
577	26	38.2	431	1	ZTEC6	H+-transporting tw	650	26	38.2	550	2	AB2000	probable membrane
578	26	38.2	431	2	AB0852	alpha-ketoglutarat	651	26	38.2	555	2	S56946	hypothetical prote
579	26	38.2	432	2	D85905	alpha-ketoglutarat	652	26	38.2	567	2	D98253	oxidoreductase, GM
580	26	38.2	432	2	JN0080	alpha-ketoglutarat	653	26	38.2	577	2	T14315	exodeoxyribonuclea
581	26	38.2	432	2	F91060	alpha-ketoglutarat	654	26	38.2	579	2	H87451	exodeoxyribonuclea
582	26	38.2	432	2	A85436	APETALA2 protein l	655	26	38.2	581	2	B81107	probable polypepti
583	26	38.2	434	2	AF0585	citrate-proton sym	656	26	38.2	581	2	B81909	exodeoxyribonuclea
584	26	38.2	434	2	JQ0576	citrate carrier pr	657	26	38.2	589	2	T42244	probable polypepti
585	26	38.2	435	2	E82848	alpha-ketoglutarat	658	26	38.2	591	2	F86445	hypothetical prote
586	26	38.2	435	2	H69607	probable sugar tra	659	26	38.2	592	2	F86242	unknown protein, 9
587	26	38.2	437	2	G97630	MFS permease [limp	660	26	38.2	613	2	JC7992	negatively regulat
588	26	38.2	437	2	AB2854	MFS permease (proline/	661	26	38.2	614	2	T29902	hypothetical prote
589	26	38.2	438	2	C90473	permease (proline/	662	26	38.2	617	2	F71359	proline-tRNA ligas
590	26	38.2	443	2	JQ1527	alpha-amylase (EC	663	26	38.2	662	2	T46623	hypothetical prote
591	26	38.2	445	2	S19990	alpha-amylase (EC	664	26	38.2	666	2	B70803	hypothetical prote
592	26	38.2	447	2	C84306	hypothetical prote	665	26	38.2	678	2	H71816	probable type II D
593	26	38.2	447	2	B64152	conserved hypothet	666	26	38.2	698	2	E85369	hypothetical prote
594	26	38.2	449	2	A41738	neuropeptide y rec	667	26	38.2	698	2	T10682	NADH2 dehydrogena
595	26	38.2	449	2	AB2887	MFS permease [limp	668	26	38.2	702	2	T12624	catalase (EC 1.11.
596	26	38.2	456	2	T06589	3-methyl-2-oxobuta	669	26	38.2	726	1	CSECHP	catalase, hydroper
597	26	38.2	458	2	A46366	galactokinase (EC	670	26	38.2	726	2	C86085	hydriperoxidase HP
598	26	38.2	458	2	T01969	potassium transpor	671	26	38.2	726	2	G91237	primosomal protein
599	26	38.2	458	2	E70145	aminopeptidase I (672	26	38.2	732	2	F91236	primosomal protein
600	26	38.2	459	2	JC6520	interferon regulat	673	26	38.2	732	2	F86083	primosomal replica
601	26	38.2	461	2	AE3208	MFS permease [limp	674	26	38.2	732	2	A35505	probable oxidoredu
602	26	38.2	461	2	H84099	cell wall-binding	675	26	38.2	747	2	B95363	hypothetical prote
603	26	38.2	462	2	T15543	hypothetical prote	676	26	38.2	753	2	T19338	hypothetical prote
604	26	38.2	463	2	A40013	phosphomannomutase	677	26	38.2	754	2	S75113	catalase (EC 1.11.
605	26	38.2	463	2	H82979	phosphomannomutase	678	26	38.2	768	2	S52684	probable membrane
606	26	38.2	467	2	B65020	hypothetical prote	679	26	38.2	770	2	S00643	anthranilate synth
607	26	38.2	467	2	A91043	hypothetical prote	680	26	38.2	770	2	S11161	anthranilate synth
608	26	38.2	467	2	D85887	hypothetical prote	681	26	38.2	771	1	WMVZ9J	ribonucleoside-dip
609	26	38.2	472	2	AE2838	conserved hypothet	682	26	38.2	771	1	WZVZH4	ribonucleoside-dip
610	26	38.2	472	2	G97615	hypothetical prote	683	26	38.2	771	2	T28496	ribonucleoside-dip
611	26	38.2	475	2	T39359	probable udp-n-ace	684	26	38.2	771	2	B36843	ribonucleoside-dip
612	26	38.2	476	2	AE1829	hypothetical prote	685	26	38.2	771	2	H72157	L4L protein - vari
613	26	38.2	477	2	G97662	benzoate transport	686	26	38.2	781	2	F82584	catalase/peroxidas

687	26	38.2	800	2	AD3129	conserved hypothet	760	25	36.8	111	2	AB2842	conserved hypothet
688	26	38.2	808	2	E64914	dimethylsulfoxide	761	25	36.8	114	2	S11952	hypothetical prote
689	26	38.2	808	2	E90915	probable oxidoredu	762	25	36.8	119	1	PSOXA	phospholipase A2 (
690	26	38.2	808	2	B85764	probable dimethyl	763	25	36.8	126	2	AF2880	hypothetical prote
691	26	38.2	812	2	AE0680	hypothetical prote	764	25	36.8	127	2	B89778	conserved hypothet
692	26	38.2	815	2	E98158	translation elonga	765	25	36.8	129	2	T20081	hypothetical prote
693	26	38.2	819	2	S43748	probable Na/H anti	766	25	36.8	129	2	T21818	hypothetical prote
694	26	38.2	821	2	B84509	hypothetical prote	767	25	36.8	131	1	WEBR41	pertussis toxin ch
695	26	38.2	825	2	T00818	fructose phosphotr	768	25	36.8	132	1	LZMK	lysozyme (EC 3.2.1
696	26	38.2	827	1	S10639	pled protein - Syn	769	25	36.8	132	2	G97202	hypothetical prote
697	26	38.2	829	2	S75776	hypothetical prote	770	25	36.8	133	2	T17300	hypothetical prote
698	26	38.2	832	2	B96702	chitinase VC1952 l	771	25	36.8	134	2	AH2645	conserved hypothet
699	26	38.2	833	2	T24682	hypothetical prote	772	25	36.8	136	2	A69521	conserved hypothet
700	26	38.2	846	2	C82135	hypothetical prote	773	25	36.8	139	2	A38744	lysozyme (EC 3.2.1
701	26	38.2	846	2	H70599	ferrichrome-iron r	774	25	36.8	140	2	AE2689	conserved hypothet
702	26	38.2	857	2	AC2132	autotransporter pr	775	25	36.8	142	2	H97470	hypothetical prote
703	26	38.2	868	2	AF3204	probable receptor-	776	25	36.8	145	2	H57427	hypothetical prote
704	26	38.2	890	2	E84846	subtilisin-like pr	777	25	36.8	148	2	S65981	hypbyp protein - Bac
705	26	38.2	896	2	G96946	subtilisin-like pr	778	25	36.8	149	2	B75449	conserved hypothet
706	26	38.2	899	2	G02428	SAP155 protein - y	779	25	36.8	150	2	F69714	spore formation pr
707	26	38.2	905	2	S56295	subtilisin-like pr	780	25	36.8	150	2	T38838	hypothetical prote
708	26	38.2	915	1	A48225	SAP155 protein - y	781	25	36.8	151	2	H25973	hypothetical prote
709	26	38.2	915	2	JC6148	subtilisin-like pr	782	25	36.8	152	1	H25973	hypothetical prote
710	26	38.2	964	2	T05382	hypothetical prote	783	25	36.8	155	2	AE2487	transcription regu
711	26	38.2	970	2	JQ0302	hypothetical 112K	784	25	36.8	158	2	F87545	spou rRNA methylas
712	26	38.2	985	2	S59330	Na+/H+-exchanging	785	25	36.8	160	2	F87307	hypothetical prote
713	26	38.2	992	2	JQ1165	Env protein - Maed	786	25	36.8	162	2	T49420	hypothetical prote
714	26	38.2	998	2	S77225	sensory transducti	787	25	36.8	164	2	A87556	ribosomal protein
715	26	38.2	1013	2	A87304	TonB-dependent rec	788	25	36.8	165	1	JN0778	ribosomal protein
716	26	38.2	1036	2	T31673	N-acetylglucosamin	789	25	36.8	165	1	R7RT12	ribosomal protein
717	26	38.2	1062	2	B26330	hypothetical prote	790	25	36.8	165	2	S35531	hypothetical prote
718	26	38.2	1103	2	A85189	disease resistance	791	25	36.8	165	2	T31150	urease accessory p
719	26	38.2	1170	2	A53612	laminin Blk chain	792	25	36.8	167	2	E83034	hypothetical prote
720	26	38.2	1204	2	S62506	alpha-glucan synth	793	25	36.8	169	2	S60891	hypothetical prote
721	26	38.2	1234	2	B36186	I factor protein 2	794	25	36.8	171	2	G70636	hypothetical prote
722	26	38.2	1371	2	H82024	probable periplasm	795	25	36.8	171	2	G81823	hypothetical prote
723	26	38.2	1402	2	S62557	probable calcium-t	796	25	36.8	174	2	B85940	hypothetical prote
724	26	38.2	1404	1	A48196	protein-tyrosine k	797	25	36.8	178	1	R5RT11	ribosomal protein
725	26	38.2	1405	2	H81003	conserved hypothet	798	25	36.8	178	2	S29383	hish protein - Zym
726	26	38.2	1445	2	A59437	KIAA1204 protein l	799	25	36.8	179	2	D98265	hypothetical prote
727	26	38.2	1548	2	S34583	serine proteinase	800	25	36.8	183	2	AE3019	conserved hypothet
728	26	38.2	1662	2	T18540	moFA protein precu	801	25	36.8	184	2	S60245	ribosomal protein
729	26	38.2	1713	2	A55347	adhesive ligand ep	802	25	36.8	184	2	A82446	hypothetical prote
730	26	38.2	1745	2	S44816	F44E2.1 protein -	803	25	36.8	185	2	D84538	amine dehydrogenas
731	26	38.2	1887	2	S61703	fatty-acid synthas	804	25	36.8	186	1	DEPSNL	hypothetical lipop
732	26	38.2	2265	1	FNBO	fibronectin - bovi	805	25	36.8	186	2	G81093	amine dehydrogenas
733	26	38.2	2272	2	T18572	gag, pol and env p	806	25	36.8	186	2	H81846	hypothetical prote
734	26	38.2	2386	1	FNHU	fibronectin precur	807	25	36.8	187	2	T10073	amine dehydrogenas
735	26	38.2	2412	1	JQ1537	genome polyprotein	808	25	36.8	188	1	JH0661	amine dehydrogenas
736	26	38.2	2467	2	D71437	probable resistanc	809	25	36.8	188	2	G75326	amine dehydrogenas
737	26	38.2	2524	2	A35844	Xotch protein - Af	810	25	36.8	188	2	F96803	hypothetical prote
738	26	38.2	2812	2	T43271	phosphotidylinosit	811	25	36.8	191	2	T29860	hypothetical prote
739	26	38.2	2957	2	T33152	hypothetical prote	812	25	36.8	196	2	T30978	hypothetical prote
740	26	38.2	3712	2	S18253	laminin alpha-1 ch	813	25	36.8	196	2	H88445	protein C26E6.1 l1
741	26	38.2	5327	2	T13564	microtubule-associ	814	25	36.8	196	2	H88445	conserved hypothet
742	26	38.2	8563	2	T30226	polyketide synthas	815	25	36.8	198	2	AB3182	hypothetical prote
743	25.5	37.5	125	2	T16247	hypothetical prote	816	25	36.8	201	2	F72390	hypothetical prote
744	25.5	37.5	231	2	S25753	Ig lambda chain -	817	25	36.8	202	2	H70760	probable lipoprote
745	25.5	37.5	341	2	S09913	hypothetical prote	818	25	36.8	204	2	T51981	proteasome endopep
746	25.5	37.5	406	2	T23898	hypothetical prote	819	25	36.8	204	2	F86350	hypothetical prote
747	25.5	37.5	428	2	A83494	hypothetical prote	820	25	36.8	207	2	T20391	hypothetical prote
748	25.5	37.5	430	2	T23899	hypothetical prote	821	25	36.8	209	2	T19025	hypothetical prote
749	25.5	37.5	630	2	A49656	estrogen-responsiv	822	25	36.8	212	2	G75359	conserved hypothet
750	25.5	37.5	1079	2	F82447	pyruvate-flavoredo	823	25	36.8	213	2	S72625	hypothetical prote
751	25	36.8	40	2	B31791	sarcotoxin ID - fl	824	25	36.8	214	2	I40768	probable lipoprote
752	25	36.8	60	2	S68769	short neurotoxin -	825	25	36.8	214	2	S74854	hypothetical prote
753	25	36.8	68	2	AD2576	hypothetical prote	826	25	36.8	215	2	AB3358	probable carnitine
754	25	36.8	75	2	B28186	nifu protein - Nos	827	25	36.8	219	2	A70314	deoxyribose-phosph
755	25	36.8	79	2	S07562	ribosomal protein	828	25	36.8	220	2	AH3231	conjugal transfer
756	25	36.8	79	2	AC2103	hypothetical prote	829	25	36.8	222	2	T00654	hypothetical prote
757	25	36.8	111	2	D81780	probable integral	830	25	36.8	223	2	T16335	hypothetical prote
758	25	36.8	111	2	A81204	multidrug resistan	831	25	36.8	223	2	E75390	phage shock protei
759	25	36.8	111	2	C97619	hypothetical prote	832	25	36.8	223	2	T05755	hypothetical prote

833	25	36.8	224	2	T16705	hypothetical prote	906	25	36.8	316	2	C81097	thioredoxin reduct
834	25	36.8	226	2	S76020	endopeptidase Clp	907	25	36.8	316	2	E81845	thioredoxin-disulf
835	25	36.8	226	2	AD3282	phosphate regulon	908	25	36.8	316	2	I50151	acidic ribosomal p
836	25	36.8	227	2	E75066	probable translati	909	25	36.8	316	2	B64304	hypothetical prote
837	25	36.8	227	2	D71166	hypothetical prote	910	25	36.8	319	2	G84241	hypothetical prote
838	25	36.8	242	2	S62017	phenylacrylic acid	911	25	36.8	320	2	S69547	transcription init
839	25	36.8	242	2	F30315	methyl viologen-re	912	25	36.8	320	2	S38670	chitinase (EC 3.2.
840	25	36.8	242	2	AC0131	probable copper ho	913	25	36.8	320	2	AE2588	mutR/nudix family
841	25	36.8	243	2	S42533	uroporphyrinogen I	914	25	36.8	320	2	E97370	NADH pyrophosphat
842	25	36.8	244	2	AC2751	transcription regu	915	25	36.8	322	2	G97396	cysteine synthase
843	25	36.8	244	2	C97532	probable transcrip	916	25	36.8	322	2	AH2614	characterized Fe-
844	25	36.8	247	2	T28865	hypothetical prote	917	25	36.8	324	2	B97298	probable cytochrom
845	25	36.8	248	2	B72240	deoxyribose-phosph	918	25	36.8	327	2	B95960	hypothetical prote
846	25	36.8	248	2	D69073	nitrate assimilati	919	25	36.8	327	2	AC2779	hypothetical prote
847	25	36.8	251	2	T42005	conserved hypothet	920	25	36.8	327	2	G97558	hypothetical prote
848	25	36.8	252	1	JN0392	matrix protein M1	921	25	36.8	327	2	G96833	hypothetical prote
849	25	36.8	252	1	MEIV	matrix protein M1	922	25	36.8	328	2	S42593	hypothetical prote
850	25	36.8	252	1	MEIV1K	matrix protein M1	923	25	36.8	330	2	D70348	ADP-ribosylglycohy
851	25	36.8	252	1	PN0086	matrix protein M1	924	25	36.8	330	2	A87662	conserved hypothet
852	25	36.8	252	1	B45539	matrix protein M1	925	25	36.8	332	2	E81665	proteinase IV, pro
853	25	36.8	252	1	MEIV1M	matrix protein M1	926	25	36.8	332	2	G83270	beta-N-acetyl-D-gl
854	25	36.8	252	1	MEIV61	matrix protein M1	927	25	36.8	334	2	E85775	hypothetical prote
855	25	36.8	252	1	MEIVC	matrix protein M1	928	25	36.8	334	2	A99927	hypothetical prote
856	25	36.8	252	1	MEIVMS	matrix protein M1	929	25	36.8	334	2	F64925	ynhG protein - Esc
857	25	36.8	252	1	PN0083	matrix protein M1	930	25	36.8	335	2	T52577	gibberellin 2beta-
858	25	36.8	252	2	S04058	matrix protein M1	931	25	36.8	335	2	B45511	chitinase (EC 3.2.
859	25	36.8	252	2	S04050	matrix protein M1	932	25	36.8	336	2	T20815	hypothetical prote
860	25	36.8	252	2	T09279	matrix protein M1	933	25	36.8	336	2	H82654	3-oxoacyl-[ACP] sy
861	25	36.8	252	2	S04056	matrix protein M1	934	25	36.8	339	1	RRVOBM	RNA-directed RNA p
862	25	36.8	252	2	S04052	matrix protein M1	935	25	36.8	339	1	RRVQCM	RNA-directed RNA p
863	25	36.8	252	2	S14616	matrix protein M1	936	25	36.8	340	2	S69194	N4-(beta-N-acetyl
864	25	36.8	252	2	S07429	matrix protein M1	937	25	36.8	341	2	I61725	natural killer ass
865	25	36.8	252	2	S04054	matrix protein M1	938	25	36.8	341	2	T16091	hypothetical prote
866	25	36.8	256	2	E95912	probable acetyltra	939	25	36.8	342	1	T24660	hypothetical phosph
867	25	36.8	258	2	G65054	hypothetical prote	940	25	36.8	343	2	JC7958	galaxin precursor
868	25	36.8	260	2	AG2658	conserved hypothet	941	25	36.8	344	2	T19367	cysteine synthase
869	25	36.8	260	2	B53422	peptidylprolyl iso	942	25	36.8	346	2	T51424	hypothetical prote
870	25	36.8	264	2	AE2274	hypothetical prote	943	25	36.8	346	2	H84751	probable sulphate-
871	25	36.8	265	2	D84198	endonuclease III l	944	25	36.8	348	2	G86985	natural killer cel
872	25	36.8	265	2	T26217	hypothetical prote	945	25	36.8	348	2	A56247	hypothetical prote
873	25	36.8	267	2	E81431	ABC transporter in	946	25	36.8	354	2	T23655	protein kinase (EC
874	25	36.8	267	2	B69461	hypothetical prote	947	25	36.8	355	2	PQ0207	probable dihydrol
875	25	36.8	269	2	G69845	enoyl-lacyl-carrie	948	25	36.8	358	2	S72584	probable 3'(2')5'
876	25	36.8	275	2	D97440	ATP synthase (AF10	949	25	36.8	358	2	T03305	probable retroelem
877	25	36.8	278	2	A83689	hypothetical prote	950	25	36.8	358	2	H84496	dihydrodipicolinat
878	25	36.8	279	1	P3VXY1	3a protein - cucum	951	25	36.8	359	2	T03214	hypothetical prote
879	25	36.8	279	2	C71392	movement protein -	952	25	36.8	359	2	T52383	hypothetical prote
880	25	36.8	279	2	JS0089	3A protein - cucum	953	25	36.8	360	2	G72235	probable dihydrol
881	25	36.8	281	2	E71046	probable ferredoxi	954	25	36.8	365	2	E84890	hypothetical prote
882	25	36.8	281	2	G75168	2-ketoglutarate fe	955	25	36.8	365	2	H84471	probable dihydrol
883	25	36.8	283	2	G83754	transcription regu	956	25	36.8	365	2	E97315	hypothetical prote
884	25	36.8	286	2	T26657	hypothetical prote	957	25	36.8	367	2	S48833	membrane protease
885	25	36.8	288	2	T38075	conserved hypothet	958	25	36.8	367	2	E51533	cytochrome-c3 hydr
886	25	36.8	293	2	F97774	hypothetical prote	959	25	36.8	372	2	AH0667	conserved hypothet
887	25	36.8	293	2	S46710	hypothetical prote	960	25	36.8	372	2	JC2556	alpha-1-microglobu
888	25	36.8	295	2	S60711	band-6-protein - b	961	25	36.8	372	2	G71074	probable cytochrom
889	25	36.8	298	2	C82824	cell division inhi	962	25	36.8	374	2	E90292	transport membrane
890	25	36.8	299	2	E75254	conserved hypothet	963	25	36.8	374	2	AH3522	xylose repressor l
891	25	36.8	300	1	D34443	nitrogen fixation	964	25	36.8	375	2	D97268	toxic anion resist
892	25	36.8	300	2	AD1988	conserved hypothet	965	25	36.8	377	1	WZWTM6	dihydrodipicolinat
893	25	36.8	300	2	AF3092	nitrogen fixation	966	25	36.8	378	2	AG2833	hypothetical prote
894	25	36.8	300	2	D98194	hypothetical prote	967	25	36.8	378	2	C97611	hypothetical prote
895	25	36.8	307	2	A27389	catechol 2,3-dioxy	968	25	36.8	379	2	H83727	phosphoribosylamin
896	25	36.8	308	2	T15055	dihydrodipicolinat	969	25	36.8	380	1	WZZMP	dihydrodipicolinat
897	25	36.8	308	2	T44614	cysteine synthase	970	25	36.8	382	2	S08595	trfa transcription
898	25	36.8	308	2	AF0809	probable transcrip	971	25	36.8	383	2	C65244	hypothetical 41.7
899	25	36.8	308	2	B69329	hypothetical prote	972	25	36.8	384	2	G84890	probable beta-gluc
900	25	36.8	309	2	AC1053	probable membrane	973	25	36.8	384	2	A10937	hypothetical prote
901	25	36.8	312	2	T02304	2'-hydroxyisoflavo	974	25	36.8	386	2	G84950	cystathionine gamm
902	25	36.8	312	2	AB1350	3-oxoacyl- acyl-ca	975	25	36.8	386	2	G64494	quintolone resistan
903	25	36.8	312	2	AE1720	3-oxoacyl- acyl-ca	976	25	36.8	387	2	A10511	probable metabolit
904	25	36.8	313	2	T26308	hypothetical prote	977	25	36.8	388	1	WZWTM7	dihydrodipicolinat
905	25	36.8	313	2	S61990	hypothetical prote	978	25	36.8	388	2	D84962	tryptophan synthas

979	25	36.8	388	2	C71961	succinyl-diaminopi
980	25	36.8	388	2	AC2011	hypothetical prote
981	25	36.8	389	2	C82987	probable MFS trans
982	25	36.8	393	2	S27881	beta-alanine synth
983	25	36.8	393	2	F72594	cystathionine beta
984	25	36.8	394	2	F86190	hypothetical prote
985	25	36.8	394	2	F82507	proteinase VCA0045
986	25	36.8	395	2	G70633	probable fadE7 pro
987	25	36.8	396	1	XNECD	aspartate transami
988	25	36.8	396	2	AD0616	aspartate aminotra
989	25	36.8	396	2	A85619	aspartate aminotra
990	25	36.8	396	2	C90755	aspartate aminotra
991	25	36.8	396	2	I64132	aspartate transami
992	25	36.8	396	2	AD0172	aspartate transami
993	25	36.8	397	1	PC1219	dihydroorotate oxi
994	25	36.8	397	2	C81188	aspartate transami
995	25	36.8	397	2	B81915	aspartate transami
996	25	36.8	397	2	F96680	F5114.10 [imported
997	25	36.8	397	2	G69295	oxalate/formate an
998	25	36.8	398	2	T35982	probable peptide t
999	25	36.8	399	2	AH2542	hypothetical prote
1000	25	36.8	401	2	S65044	phosphoglycerate k

ALIGNMENTS

RESULT 1

S01657 atrial natriuretic factor - laughing frog (tentative sequence) (fragment)

N;Alternate names: atriopeptin

C;Species: Rana ridibunda (laughing frog)

C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004

C;Accession: S01657; A30977

R;Lazure, C.; Ong, H.; McNicoll, N.; Netchitailo, P.; Chretien, M.; de Lean, A.; Vaudry, FEBS Lett. 238, 300-306, 1988

A;Title: The amino acid sequences of frog heart atrial natriuretic-like peptide and mamm

A;Reference number: S01657; MUID:89005705; PMID:2971573

A;Accession: S01657

A;Molecule type: protein

A;Residues: 1-30 <LAZ>

A;Cross-references: UNIPROT:P09196; UNIPARC:UPI00000351F2

A;Note: the sequence from the summary is inconsistent with that from Fig. 3 in lacking r

C;Superfamily: natriuretic peptide A precursor

Query Match 82.4%; Score 56; DB 2; Length 30;
Best Local Similarity 58.8%; Pred. No. 2.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXGC 17
Db 11 CFGSRIDRIGAQSGMGC 27

RESULT 2

S14872 atrial natriuretic peptide precursor - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004

C;Accession: S14872

R;Maegert, H.J.; Hanke, M.; Schmeding, G.; Teuteberg, K.; Schulz-Knappe, P.; Forssmann, submitted to the EMBL Data Library, March 1991

A;Reference number: S14872

A;Accession: S14872

A;Molecule type: mRNA

A;Residues: 1-128 <MAE>

A;Cross-references: UNIPROT:P27596; UNIPARC:UPI0000125AF9; EMBL:X58562; NID:G49543; PIDN

A;Experimental source: heart atria, adult

C;Superfamily: natriuretic peptide A precursor

C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation

F;1-98/Domain: signal sequence #status predicted <SIG>

F;99-128/Product: atrial natriuretic peptide #status predicted <MAT>

F;105-121/Disulfide bonds: #status predicted

Query Match 82.4%; Score 56; DB 2; Length 128;
Best Local Similarity 58.8%; Pred. No. 9.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXGC 17
Db 105 CFGGRMDRIGAQSSIGC 121

RESULT 3

JQ0947 atrial natriuretic peptide precursor - bullfrog

N;Alternate names: ANP; atrial natriuretic factor (ANF)

N;Contains: atrial natriuretic peptide-21; atrial natriuretic peptide-24

C;Species: Rana catesbeiana (bullfrog)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JQ0947; A31510

R;Kojima, M.

submitted to JPIID, May 1991

A;Reference number: JQ0947

A;Accession: JQ0947

A;Molecule type: mRNA

A;Residues: 1-145 <KOJ>

A;Cross-references: UNIPROT:P18909; UNIPARC:UPI0000125AF9

R;Sakata, J.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 155, 1338-1345, 1988

A;Title: Identification of new atrial natriuretic peptides in frog heart.

A;Reference number: A31510; MUID:89025806; PMID:2972279

A;Accession: A31510

A;Molecule type: protein

A;Residues: 122-145 <SAK>

A;Cross-references: UNIPARC:UPI00000351EF

C;Comment: In mammals, several active peptides may be derived from the prohormone.

C;Superfamily: natriuretic peptide A precursor

C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-121/Domain: propeptide #status predicted <PRO>

F;122-145/Product: atrial natriuretic peptide-24 #status experimental <M24>

F;125-145/Product: atrial natriuretic peptide-21 #status experimental <M21>

F;125-141/Disulfide bonds: #status predicted

Query Match 82.4%; Score 56; DB 1; Length 145;
Best Local Similarity 58.8%; Pred. No. 0.0001;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXGC 17
Db 125 CFGSRIDRIGAQSGMGC 141

RESULT 4

JT0581 natriuretic peptide type C - chicken

C;Species: Gallus gallus (chicken)

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C;Accession: JT0581

R;Arimura, J.J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 174, 142-148, 1991

A;Title: Isolation and identification of C-type natriuretic peptide in chicken brain.

A;Reference number: JT0581; MUID:9113186; PMID:1989595

A;Accession: JT0581

A;Molecule type: protein

A;Residues: 1-22 <ARI>

A;Cross-references: UNIPROT:P21805; UNIPARC:UPI0000035211

A;Experimental source: brain

C;Superfamily: natriuretic peptide A precursor

C;Keywords: diuretic; hormone; natriuretic; osmoregulation

Query Match 80.9%; Score 55; DB 2; Length 22;
Best Local Similarity 58.8%; Pred. No. 3.1e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 6 CFGVKLDRI GMSGLGC 22

RESULT 5

brain natriuretic peptide - Japanese eel
A35418
C/Species: Anguilla japonica (Japanese eel)
C/Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C/Accession: A35418
R/Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.; Sakakibara, S.; Takao, T.; Shi
Biochem. Biophys. Res. Commun. 170, 883-891, 1990
A/Title: Amino acid sequence and relative biological activity of a natriuretic peptide
A/Reference number: A35418; MUID:90343814; PMID:2143379
A/Accession: A35418
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-22 <TAK>
A/Cross-references: UNIPROT:P18145; UNIPARC:UPI000003520A
C/Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 22;
Best Local Similarity 58.8%; Pred. No. 3.1e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 6 CFGVKLDRI GMSGLGC 22

RESULT 6

C-type natriuretic peptide - frog
A36399
C/Species: Ranidae gen. sp. (frog)
C/Date: 01-Feb-1991 #sequence_revision 01-Feb-1991 #text_change 09-Jul-2004
C/Accession: A36399
R/Yoshihara, A.; Kozawa, H.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 173, 591-598, 1990
A/Title: Isolation and sequence determination of frog C-type natriuretic peptide.
A/Reference number: A36399; MUID:91083642; PMID:2148082
A/Accession: A36399
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-22 <YOS>
A/Cross-references: UNIPROT:P20968; UNIPARC:UPI00001566AB
C/Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 22;
Best Local Similarity 58.8%; Pred. No. 3.1e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 6 CFGVKLDRI GMSGLGC 22

RESULT 7

brain natriuretic peptide - pig
JC1081
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 16-Feb-1997
C/Accession: JC1081
R/Chen, H.; Zhang, J.; Wang, Q.S.; Cui, H.; Tang, J.
J. Fudan Univ. (Natur. Sci.) 30, 413-416, 1991
A/Title: Chemical synthesis and cloning of the porcine brain natriuretic gene.
A/Reference number: JC1081
A/Accession: JC1081
A/Molecule type: DNA
A/Residues: 1-27 <CHE>
A/Cross-references: UNIPARC:UPI0000176582
A/Note: The translation of the start codon ATG is not given in this paper
C/Genetics:

A/Gene: bnp
C/Superfamily: natriuretic peptide A precursor
C/Keywords: brain; natriuretic

Query Match 80.9%; Score 55; DB 2; Length 27;
Best Local Similarity 58.8%; Pred. No. 3.7e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 5 CFGRRLDRI GMSGLGC 21

RESULT 8

atrial natriuretic factor - Japanese eel
A33431
C/Species: Anguilla japonica (Japanese eel)
C/Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C/Accession: A33431
R/Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.; Sakakibara, S.
Biochem. Biophys. Res. Commun. 164, 537-543, 1989
A/Title: Amino acid sequence and relative biological activity of eel atrial natriureti
A/Reference number: A33431; MUID:90026430; PMID:2529857
A/Accession: A33431
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-27 <TAK>
A/Cross-references: UNIPROT:P18144; UNIPARC:UPI00000351F9
C/Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 27;
Best Local Similarity 58.8%; Pred. No. 3.7e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 7 CFGVKLDRI GMSGLGC 23

RESULT 9

ventricular natriuretic peptide - Japanese eel
S15821
C/Species: Anguilla japonica (Japanese eel)
C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C/Accession: S15821
R/Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.; Sakakibara, S.
FEBS Lett. 282, 317-320, 1991
A/Title: A novel natriuretic peptide isolated from eel cardiac ventricles.
A/Reference number: S15821; MUID:91243821; PMID:1828035
A/Accession: S15821
A/Molecule type: protein
A/Residues: 1-36 <FEB>
A/Cross-references: UNIPROT:P22642; UNIPARC:UPI0000125AF6
C/Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 36;
Best Local Similarity 58.8%; Pred. No. 4.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 6 CFGRRMDRI GMSGLGC 22

RESULT 10

lebetin 2 isoform alpha - Vipera lebetina
S71381
C/Species: Vipera lebetina
C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C/Accession: S71381; S71382; S71379
R/Barbouche, R.; Marrakchi, N.; Mansuelle, P.; Krifi, M.; Fenouillet, E.; Rochat, H.; i
FEBS Lett. 392, 6-10, 1996
A/Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isol

A;Reference number: S71379; MUID:96354866; PMID:8769304
A;Accession: S71381
A;Molecule type: protein
A;Residues: 1-38 <BAR>
A;Cross-references: UNIPROT:Q7LZ09; UNIPARC:UPI0000030733
A;Experimental source: venom
A;Accession: S71382
A;Molecule type: protein
A;Residues: 2-38 <BA2>
A;Cross-references: UNIPARC:UPI0000030734
A;Experimental source: venom
A;Accession: S71379
A;Molecule type: protein
A;Residues: 1-13 <BA3>
A;Cross-references: UNIPARC:UPI000003072F
A;Experimental source: venom
C;Keywords: anticoagulant; venom
F;14-30/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 2; Length 38;
Best Local Similarity 58.8%; Pred. No. 5.1e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 14 CFGHKIDRIGSHSGLGC 30

RESULT 11

A41403
aldosterone secretion inhibitory factor precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41403; A30976
R;Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; De Lean, A.; Ong, H.
Mol. Endocrinol. 3, 1823-1829, 1989
A;Title: Purification and primary structure of pro-aldosterone secretion inhibitory fact
A;Reference number: A41403; MUID:90114187; PMID:2532709
A;Accession: A41403
A;Molecule type: protein
A;Residues: 1-103 <NGU>
A;Cross-references: UNIPROT:P13204; UNIPARC:UPI0000125AD9
R;Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; Ong, H.; de Lean, A.
Endocrinology 124, 1591-1593, 1989
A;Title: Aldosterone secretion inhibitory factor: a novel neuropeptide in bovine chromaf
A;Reference number: A30976; MUID:89136947; PMID:2537187
A;Accession: A30976
A;Molecule type: protein
A;Residues: 69-103 <NG2>
A;Cross-references: UNIPARC:UPI0000176580
C;Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 103;
Best Local Similarity 58.8%; Pred. No. 0.00012;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 81 CFGRRIDRIGSLSGLGC 97

RESULT 12

B36736
brain natriuretic peptide - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
C;Accession: B36736
R;Seilhamer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki,
Biochem. Biophys. Res. Commun. 165, 650-658, 1989
A;Title: Human and canine gene homologs of porcine brain natriuretic peptide.
A;Reference number: A36736; MUID:90088474; PMID:2597152
A;Accession: B36736
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-105 <SEI>
A;Cross-references: UNIPROT:P16859; UNIPARC:UPI0000176581; GB:M31777
C;Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 105;
Best Local Similarity 58.8%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 83 CFGRRIDRIGSLSGLGC 99

RESULT 13

S15822
natriuretic peptide type C - smaller spotted catshark
C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S15822
R;Suzuki, R.; Takahashi, A.; Hazon, N.; Takei, Y.
FEBS Lett. 282, 321-325, 1991
A;Title: Isolation of high-molecular-weight C-type natriuretic peptide from the heart of
A;Accession: S15822; MUID:91243822; PMID:1828036
A;Molecule type: protein
A;Residues: 1-115 <FEB>
A;Cross-references: UNIPROT:P23259; UNIPARC:UPI0000125AE3
C;Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 1; Length 115;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 99 CFGVKLDRIGAMSGLC 115

RESULT 14

B54119
C-type natriuretic peptide II precursor - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: B54119
R;Kojima, M.; Ohyama, Y.; Miyamoto, K.; Minamino, N.; Kangawa, K.; Matsuo, H.
J. Biol. Chem. 269, 13136-13140, 1994
A;Title: Cloning and characterization of a novel natriuretic peptide in frog (Rana cates
A;Reference number: A54119; MUID:94230409; PMID:8175740
A;Accession: B54119
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <KOJ>
A;Cross-references: UNIPROT:P40756; UNIPARC:UPI0000125AEA; GB:D17414; NID:G397835; PIDN
A;Note: authors translated the codon AAA for residue 89 as Ile
C;Superfamily: natriuretic peptide C precursor

Query Match 80.9%; Score 55; DB 2; Length 118;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXGC 17
||| |||| | ||
Db 102 CFGKLDRIGAMSGLC 118

RESULT 15

A30162
brain natriuretic factor precursor - rat
N;Alternate names: brain natriuretic peptide; cardiac natriuretic factor; iso-atrial nat
N;Contains: brain natriuretic factor BNP-45
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A30162; A35691; A54893; A32918; A32919; A33253; A60735; I57704; A33252
R;Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 159, 1420-1426, 1989
A;Title: Cloning and sequence analysis of cDNA encoding a precursor for rat brain natriu
A;Reference number: A30162; MUID:89193742; PMID:2522776
A;Accession: A30162
A;Molecule type: mRNA
A;Residues: 1-121 <KOU>
A;Cross-references: UNIPROT:P13205; UNIPARC:UPI0000125ADC; GB:M25297; NID:g602483; PIDN:
R;Roy, R.N.; Flynn, T.G.
Biochem. Biophys. Res. Commun. 171, 416-423, 1990
A;Title: Organization of the gene for iso-rAMP, a rat B-type natriuretic peptide.
A;Reference number: A35691; MUID:90365739; PMID:2144113
A;Accession: A35691
A;Molecule type: DNA
A;Residues: 1-14, 'V', 16-121 <ROY>
A;Cross-references: UNIPARC:UPI00001709D6; GB:M60731; NID:g204985; PIDN:AAA41456.1; PID:
A;Note: the authors translated the codon GTT for residue 15 as Leu
R;Thuermer, D.J.; Hanford, D.S.; Glembocki, C.C.
J. Biol. Chem. 269, 17772-17775, 1994
A;Title: Regulation of rat brain natriuretic peptide transcription. A potential role for
A;Reference number: A54893; MUID:94299479; PMID:8027030
A;Accession: A54893
A;Molecule type: DNA
A;Residues: 1-19 <THU>
A;Cross-references: UNIPARC:UPI000000516; GB:U02972; NID:g458021; PIDN:AAA21648.1; PID:
R;Aburaya, M.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 163, 226-232, 1989
A;Title: Isolation and identification of rat brain natriuretic peptides in cardiac atriu
A;Reference number: A32918; MUID:89374230; PMID:2673236
A;Accession: A32918
A;Molecule type: protein
A;Residues: 27-121 <ABU>
A;Cross-references: UNIPARC:UPI00001733AC
R;Kambayashi, Y.; Nakao, K.; Itoh, H.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.;
Imura, H.
Biochem. Biophys. Res. Commun. 163, 233-240, 1989
A;Title: Isolation and sequence determination of rat cardiac natriuretic peptide.
A;Reference number: A32919; MUID:89374231; PMID:2528349
A;Accession: A32919
A;Molecule type: protein
A;Residues: 77-121 <KAM>
A;Cross-references: UNIPARC:UPI000003520F
R;Flynn, T.G.; Brar, A.; Tremblay, L.; Sarda, I.; Lyons, C.; Jennings, D.B.
Biochem. Biophys. Res. Commun. 161, 830-837, 1989
A;Title: Isolation and characterization of iso-rAMP, a new natriuretic peptide from rat
A;Reference number: A33253; MUID:89286593; PMID:2525380
A;Accession: A33253
A;Molecule type: protein
A;Residues: 77-119, 'Q', 121 <FLY>
A;Cross-references: UNIPARC:UPI00001733AD
R;Nakao, K.; Itoh, H.; Kambayashi, Y.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.;
Hypertension 15, 774-778, 1990
A;Title: Rat brain natriuretic peptide. Isolation from rat heart and tissue distribution
A;Reference number: A60735; MUID:90277148; PMID:2351430
A;Accession: A60735
A;Molecule type: protein
A;Residues: 77-121 <NAK>
A;Cross-references: UNIPARC:UPI000003520F
R;Dagnino, L.; Drouin, J.; Nemer, M.
Mol. Endocrinol. 5, 1292-1300, 1991
A;Title: Differential expression of natriuretic peptide genes in cardiac and extracardia
A;Reference number: I57704; MUID:92123224; PMID:1837590
A;Accession: I57704
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-121 <RES>
A;Cross-references: UNIPARC:UPI0000125ADC; GB:M60266; NID:g204983; PIDN:AAA41455.1; PID:
C;Genetics:
A;Introns: 42/3; 117/1
C;Superfamily: natriuretic peptide A precursor
C;Keywords: cardiac muscle; heart
F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-121/Product: brain natriuretic factor #status experimental <MAT1>
F;77-121/Product: brain natriuretic factor BNP-45 #status experimental <MAT2>
Query Match 80.9%; Score 55; DB 1; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXDRIGXXSXXGC 17
DB 99 CFGKIDRIGSVSRLGC 115
RESULT 16
A49144
type-B natriuretic peptide, BNP - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A49144
R;Steinhilper, M.E.
Circ. Res. 72, 984-992, 1993
A;Title: Structure, expression, and genomic mapping of the mouse natriuretic peptide t
A;Reference number: A49144; MUID:93238395; PMID:8097440
A;Accession: A49144
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-121 <STE>
A;Cross-references: UNIPARC:UPI0000176583; GB:S58667; NID:g299794; PIDN:AAB26344.1; PI
A;Experimental source: BALB/c
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:130161, NCBIPI:130162)
C;Superfamily: natriuretic peptide A precursor
Query Match 80.9%; Score 55; DB 2; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXDRIGXXSXXGC 17
DB 99 CFGKIDRIGSVSRLGC 115
RESULT 17
I49548
brain natriuretic peptide - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49548
R;Ogawa, Y.; Itoh, H.; Tamura, N.; Suga, S.; Yoshimasa, T.; Uehira, M.; Matsuda, S.; Si
J. Clin. Invest. 93, 1911-1921, 1994
A;Title: Molecular cloning of the complementary DNA and gene that encode mouse brain n
A;Reference number: I49548; MUID:94237953; PMID:8182124
A;Accession: I49548
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-121 <RES>
A;Cross-references: UNIPROT:P40753; UNIPARC:UPI0000000CE3; GB:D16497; NID:g4936559; PIDN
C;Genetics:
A;Gene: BNP
A;Introns: 42/3; 117/1
C;Superfamily: natriuretic peptide A precursor
Query Match 80.9%; Score 55; DB 2; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXDRIGXXSXXGC 17
DB 99 CFGKIDRIGSVSRLGC 115
RESULT 18
A36155
natriuretic peptide C precursor - pig

C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A36155; A35423; A34642
R;Tawaragi, Y.; Fuchimura, K.; Nakazato, H.; Tanaka, S.; Minamino, N.; Kangawa, K.; Mats
Biochem. Biophys. Res. Commun. 172, 627-632, 1990
A;Title: Gene and precursor structure of porcine C-type natriuretic peptide.
A;Reference number: A36155; MUID:91054475; PMID:2146957
A;Accession: A36155
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-126 <TAW>
A;Cross-references: UNIPROT:P18104; UNIPARC:UPI0000125AE0; EMBL:M64758; NID:g309789; PID
R;Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 170, 973-979, 1990
A;Title: N-terminally extended form of C-type natriuretic peptide (CNP-53) identified in
A;Reference number: A35423; MUID:90343827; PMID:2383278
A;Accession: A35423
A;Status: preliminary
A;Molecule type: protein
A;Residues: 74-126 <MIN>
A;Cross-references: UNIPARC:UPI0000035212
R;Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 168, 863-870, 1990
A;Title: C-type natriuretic peptide (CNP): a new member of natriuretic peptide family id
A;Reference number: A34642; MUID:90241265; PMID:2139780
A;Accession: A34642
A;Status: preliminary
A;Molecule type: protein
A;Residues: 105-126 <SUD>
A;Cross-references: UNIPARC:UPI0000033C90
C;Superfamily: natriuretic peptide C precursor
C;Keywords: disulfide bond; diuretic; hormone; natriuretic; osmoregulation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;74-126/Product: natriuretic peptide C-53 #status experimental <C53>
F;98-126/Product: natriuretic peptide C-29 #status predicted <C29>
F;105-126/Product: natriuretic peptide C-22 #status experimental <C22>
F;110-126/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXGC 17
Db 110 CFGKLDRIGSMGLGC 126

RESULT 19
AMHUC
natriuretic peptide C precursor [validated] - human
N;Alternate names: natriuretic factor C
N;Contains: natriuretic peptide C-22; natriuretic peptide C-29; natriuretic peptide C-53
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: JT0567; JC1361; T54400
R;Tawaragi, Y.; Fuchimura, K.; Tanaka, S.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 175, 645-651, 1991
A;Title: Gene and precursor structures of human C-type natriuretic peptide.
A;Reference number: JT0567; MUID:91207363; PMID:2018508
A;Accession: JT0567
A;Molecule type: DNA
A;Residues: 1-126 <TAW>
A;Cross-references: UNIPROT:P23582; UNIPARC:UPI0000033C91; GB:M64710; NID:g180676; PIDN:
R;Ishizaka, Y.; Kangawa, K.; Minamino, N.; Ishii, K.; Takano, S.; Eto, T.; Matsuo, H.
Biochem. Biophys. Res. Commun. 189, 697-704, 1992
A;Title: Isolation and identification of C-type natriuretic peptide in human monocytic c
A;Reference number: JC1361; MUID:93112033; PMID:1472040
A;Accession: JC1361
A;Molecule type: protein
A;Residues: 98-109, 'X', 111-118 <ISH>
A;Cross-references: UNIPARC:UPI00001733AE
R;Ogawa, Y.; Nakao, K.; Nakagawa, O.; Komatsu, Y.; Hosoda, K.; Suga, S.; Arai, H.; Nagat
Hypertension 19, 809-813, 1992

A;Title: Human C-type natriuretic peptide, Characterization of the gene and peptide.
A;Reference number: I54400; MUID:92275775; PMID:1339402
A;Accession: I54400
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-126 <RES>
A;Cross-references: UNIPARC:UPI0000033C91; GB:D90337; NID:g219542; PIDN:BAAL4351.1; PID
C;Genetics:
A;Gene: GDB:NPPC
A;Cross-references: GDB:250346; OMIM:600296
A;Map position: 2pter-2qter
A;Introns: 30/3
C;Superfamily: natriuretic peptide C precursor
C;Keywords: brain; diuretic; hormone; natriuretic; neuropeptide; osmoregulation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;74-126/Product: natriuretic peptide C-53 #status predicted <C53>
F;98-126/Product: natriuretic peptide C-29 #status experimental <C29>
F;105-126/Product: natriuretic peptide C-22 #status predicted <C22>
F;110-126/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXGC 17
Db 110 CFGKLDRIGSMGLGC 126

RESULT 20
A55688
natriuretic peptide c precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55688
R;Ogawa, Y.; Itoh, H.; Yoshitake, Y.; Inoue, M.; Yoshimasa, T.; Serikawa, T.; Nakao, K.
Genomics 24, 383-387, 1994
A;Title: Molecular cloning and chromosomal assignment of the mouse C-type natriuretic pe
A;Reference number: A55688; MUID:95213034; PMID:7698765
A;Accession: A55688
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-126 <OGA>
A;Cross-references: UNIPROT:Q61839; UNIPARC:UPI0000033FF3; GB:D28873; NID:g633087; PIDN
C;Genetics:
A;Gene: Nppc
C;Superfamily: natriuretic peptide C precursor

Query Match 80.9%; Score 55; DB 2; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXGC 17
Db 110 CFGKLDRIGSMGLGC 126

RESULT 21
S12988
brain natriuretic peptide type C - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S12988
R;Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
FEBS Lett. 276, 209-213, 1990
A;Title: Cloning and sequence analysis of a cDNA encoding a precursor for rat C-type nat
A;Reference number: S12988; MUID:91092420; PMID:1702395
A;Accession: S12988
A;Molecule type: mRNA
A;Residues: 1-126 <KOJ>
A;Cross-references: UNIPROT:P55207; UNIPARC:UPI0000125AE2; GB:D90219; NID:g220711; PIDN
C;Superfamily: natriuretic peptide C precursor

Query Match 80.9%; Score 55; DB 2; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 110 CFGKLDRIGMSGGLGC 126

RESULT 22
A54119
c-type natriuretic peptide I precursor - bullfrog
N:Alternate names: CNP I
C:Species: Rana catesbeiana (bullfrog)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A54119
R:Kojima, M.; Ohyama, Y.; Miyamoto, K.; Minamino, N.; Kangawa, K.; Matsuo, H.
J. Biol. Chem. 269, 13136-13140, 1994
A:Title: Cloning and characterization of a novel natriuretic peptide in frog (Rana catesbeiana)
A:Reference number: A54119; MUID:94230409; PMID:8175740
A:Accession: A54119
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KOJ>
A:Cross-references: UNIPROT:P20968; UNIPARC:UPI0000125AE1; GB:D17413; NID:G397837; PIDN:
C:Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 1; Length 129;
Best Local Similarity 58.8%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 113 CFGVKLDRIGAFSGLGC 129

RESULT 23
A31676
brain natriuretic factor precursor - pig
N:Alternate names: brain natriuretic factor 32
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C:Accession: A31676; A31517; S06359
R:Maekawa, K.; Sudoh, T.; Furusawa, M.; Minamino, N.; Kangawa, K.; Ohkubo, H.; Nakanishi, H.
Biochem. Biophys. Res. Commun. 157, 410-416, 1988
A:Title: Cloning and sequence analysis of cDNA encoding a precursor for porcine brain natriuretic factor
A:Reference number: A31676; MUID:89061744; PMID:3196348
A:Accession: A31676
A:Molecule type: mRNA
A:Residues: 1-131 <MAE>
A:Cross-references: UNIPROT:P07634; UNIPARC:UPI00001561A8; GB:M23596; NID:G535704; PIDN:
R:Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 155, 726-732, 1988
A:Title: Brain natriuretic peptide-32: N-terminal six amino acid extended form of brain natriuretic peptide
A:Reference number: A31517; MUID:88339957; PMID:3421965
A:Accession: A31517
A:Molecule type: protein
A:Residues: 100-131 <SUD>
A:Cross-references: UNIPARC:UPI000003520D
R:Sudoh, T.; Kangawa, K.; Minamino, N.; Matsuo, H.
Nature 332, 78-81, 1988
A:Title: A new natriuretic peptide in porcine brain.
A:Reference number: S06359; MUID:88156915; PMID:2964562
A:Accession: S06359
A:Molecule type: protein
A:Residues: 106-131 <SU2>
A:Cross-references: UNIPARC:UPI000003520C
C:Superfamily: natriuretic peptide A precursor
C:Keywords: brain; natriuretic
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-131/Product: brain gamma natriuretic factor #status predicted <GAM>
F:100-131/Product: brain alpha natriuretic peptide #status experimental <ALF>
F:109-125/Disulfide bonds: #status experimental

Query Match 80.9%; Score 55; DB 2; Length 131;
Best Local Similarity 58.8%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 109 CFGRRLDRIIGSLGLGC 125

RESULT 24
A33873
brain natriuretic peptide precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C:Accession: A33873; A31675
R:Porter, J.G.; Arfsten, A.; Palisi, T.; Scarborough, R.M.; Lewicki, J.A.; Seilhamer, J.
J. Biol. Chem. 264, 6689-6692, 1989
A:Title: Cloning of a cDNA encoding porcine brain natriuretic peptide.
A:Reference number: A33873; MUID:89214071; PMID:2708334
A:Accession: A33873
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <POR>
A:Cross-references: UNIPROT:P07634; UNIPARC:UPI0000125ADB; GB:M25547; GB:J04708; GB:M2222
R:Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 157, 402-409, 1988
A:Title: Isolation and identification of a high molecular weight brain natriuretic peptide
A:Reference number: A31675; MUID:89061743; PMID:3196347
A:Accession: A31675
A:Status: preliminary
A:Molecule type: protein
A:Residues: 26-131 <MIN>
A:Cross-references: UNIPARC:UPI000017657F
C:Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 131;
Best Local Similarity 58.8%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||
Db 109 CFGRRLDRIIGSLGLGC 125

RESULT 25
A61244
natriuretic peptide type C precursor - spiny dogfish
C:Species: Squalus acanthias (spiny dogfish)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A61244; I51329
R:Schofield, J.P.; Jones, D.S.C.; Forrest Jr., J.N.
Am. J. Physiol. 261, F734-F739, 1991
A:Title: Identification of C-type natriuretic peptide in heart of spiny dogfish shark (Sphyrna tiburo)
A:Reference number: A61244; MUID:92026459; PMID:1928383
A:Accession: A61244
A:Molecule type: mRNA
A:Residues: 1-135 <SCH>
A:Cross-references: UNIPROT:P41319; UNIPARC:UPI0000125AE5; EMBL:X59991; NID:G556803; PI
C:Genetics: 30/3
A:Introns: 30/3
C:Superfamily: natriuretic peptide A precursor
C:Keywords: disulfide bond; diuretic; hormone; natriuretic; osmoregulation
F:1-25/Domain: signal sequence #status predicted <SIG>
F:114-135/Product: natriuretic peptide C #status predicted <NPC>
F:119-135/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 135;
Best Local Similarity 58.8%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
||| ||| | ||

Db 119 CFGKLDRIGAMSLGC 135

RESULT 26

S14320

alpha-atrial natriuretic peptide precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S14320; A31509

R:Akizuki, N.; Kangawa, K.; Minamino, N.; Matsuo, H.

PEBS Lett. 280, 357-362, 1991

A:Title: Cloning and sequence analysis of complementary DNA encoding a precursor for chi

A:Reference number: S14320; MUID:91192169; PMID:1826483

A:Accession: S14320

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140 <AKI>

A:Cross-references: UNIPROT:P18908; UNIPARC:UPI0000125AFA; GB:X57702; NID:g63648; PIDN:C

R:Miyaata, A.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 155, 1330-1337, 1988

A:Title: Identification of a 29-amino acid natriuretic peptide in chicken heart.

A:Reference number: A31509; MUID:89025805; PMID:2972278

A:Accession: A31509

A:Molecule type: protein

A:Residues: 112-140 <MIY>

A:Cross-references: UNIPARC:UPI00000351EC

C:Superfamily: natriuretic peptide A precursor

F,118-134/Disulfide bonds: #status experimental

Query Match 80.9%; Score 55; DB 1; Length 140;

Best Local Similarity 58.8%; Pred. No. 0.00016;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXXGC 17

Db 118 CFGRRIDRIGSLGMC 134

RESULT 27

AWDC

atrial natriuretic peptide precursor - dog

N:Alternate names: ANP; atrial natriuretic polypeptide

C:Species: Canis lupus familiaris (dog)

C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004

C:Accession: A25302

R:Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato, H.; Matsuo, H.

Biochem. Biophys. Res. Commun. 132, 892-899, 1985

A:Title: Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduc

A:Reference number: A90119; MUID:86076957; PMID:2934062

A:Accession: A25302

A:Molecule type: mRNA

A:Residues: 1-149 <OIK>

A:Cross-references: UNIPROT:P07499; UNIPARC:UPI0000125AF8; GB:M12045; NID:g163900; PIDN:

C:Superfamily: natriuretic peptide A precursor

C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation

F,1-23/Domain: signal sequence #status predicted <SIG>

F,24-149/Product: gamma atrial natriuretic factor #status predicted <ANF>

F,122-149/Product: alpha atrial natriuretic peptide #status predicted <ANP>

F,128-144/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 149;

Best Local Similarity 58.8%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXXGC 17

Db 128 CFGGRMDRIGAQSGLGC 144

RESULT 28

S13107

atrial natriuretic peptide precursor - pig

N:Contains: alpha atrial natriuretic peptide; gamma atrial natriuretic factor (cardiodil

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Nov-1993 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C:Accession: S13107; A60899

R:Maegert, H.U.; Appelhans, H.; Gassen, H.G.; Forsmann, W.G.

Nucleic Acids Res. 18, 6704, 1990

A:Title: Nucleotide sequence of a porcine prepro atrial natriuretic peptide (ANP) cDNA.

A:Reference number: S13107; MUID:91067478; PMID:2147477

A:Accession: S13107

A:Molecule type: mRNA

A:Residues: 1-150 <MAE>

A:Cross-references: UNIPROT:P24259; UNIPARC:UPI0000125AFD; EMBL:X54669; NID:g1883; PIDN

R:Forsmann, W.G.; Hock, D.; Lottspeich, A.; Henschen, A.; Kreye, V.; Christmann, M.; Re

Anat. Embryol. 168, 307-313, 1983

A:Title: The right auricle of the heart is an endocrine organ. Cardiodilatin as a peptid

A:Reference number: A60899; MUID:84176555; PMID:6689515

A:Accession: A60899

A:Molecule type: protein

A:Residues: 25-54 <FOR>

A:Cross-references: UNIPARC:UPI00001733A9

C:Superfamily: natriuretic peptide A precursor

C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation

F,1-24/Domain: signal sequence #status predicted <SIG>

F,25-150/Product: gamma atrial natriuretic factor #status predicted <ANF>

F,123-150/Product: alpha atrial natriuretic peptide #status predicted <ANP>

F,129-145/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 150;

Best Local Similarity 58.8%; Pred. No. 0.00018;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGXXSXXGC 17

Db 129 CFGGRMDRIGAQSGLGC 145

RESULT 29

AWHU

natriuretic peptide A precursor [validated] - human

N:Alternate names: ANF; atrial natriuretic factor; atrial natriuretic protein; prepronat

N:Contains: atrial alpha natriuretic peptide (ANP); cardiodilatin (atrial gamma natriure

C:Species: Homo sapiens (man)

C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004

C:Accession: A22693; B22693; A01424; B29370; A32733; I58054; S14097; I39458; I39459; I39

R:Nemer, M.; Chamberland, M.; Sirolis, D.; Argentin, S.; Drouin, J.; Dixon, R.A.F.; Zivin

Nature 312, 654-656, 1984

A:Title: Gene structure of human cardiac hormone precursor, pronatriodilatin.

A:Reference number: A22693; MUID:85061626; PMID:6095118

A:Accession: A22693

A:Molecule type: DNA

A:Residues: 1-151 <NEM>

A:Cross-references: UNIPROT:P01160; UNIPARC:UPI000000DCD4; GB:X01470; NID:g28687; PIDN:

A:Accession: B22693

A:Molecule type: DNA

A:Residues: 1-151, 'RR' <NE2>

A:Cross-references: UNIPARC:UPI0000125AFC

A>Note: allelic variant with UGA termination codon replaced by CGA arginine codon

R:Oikawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.; Nakazato, H.; Kangawa, K.; Fu

Nature 309, 724-726, 1984

A:Title: Cloning and sequence analysis of cDNA encoding a precursor for human atrial nat

A:Reference number: A01424; MUID:84219799; PMID:6203042

A:Accession: A01424

A:Molecule type: mRNA

A:Residues: 1-151 <OIK>

A:Cross-references: UNIPARC:UPI000000DCD4; GB:X02043; NID:g178629; PIDN:AAB59379.1; PID

R:Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G.

Science 226, 1206-1209, 1984

A:Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.

A:Reference number: A29370; MUID:85065766; PMID:6542248

A:Accession: B29370

A:Molecule type: DNA

A:Residues: 1-64, 'D', '66-151 <SEI>

A:Cross-references: UNIPARC:UPI000016A557; GB:K02043

R:Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 118, 131-139, 1984
A/Title: Purification and complete amino acid sequence of alpha-human atrial natriuretic
A/Reference number: A32733; MUID:84128019; PMID:6230082
A/Accession: A32733
A/Molecule type: protein
A/Residues: 124-151 <KAN>
A/Cross-references: UNIPARC:UPI000002B7D3
R/Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S.
Nature 310, 699-701, 1984
A/Title: mRNA sequence for human cardiodilantin-atrial natriuretic factor precursor and
A/Reference number: 158054; MUID:84295577; PMID:6547996
A/Accession: 158054
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-151 <RES>
A/Cross-references: UNIPARC:UPI000000DCD4; GB:M30262; NID:g180181; PIDN:AAA35669.1; PID:
R/Vanneste, Y.; Michel, A.; Deschodt-Lanckman, M.
Eur. J. Biochem. 196, 281-286, 1991
A/Title: Hydrolysis of intact and Cys-Phe-cleaved human atrial natriuretic peptide in vi
A/Reference number: S14097; MUID:91176998; PMID:1826098
A/Accession: S14097
A/Molecule type: protein
A/Residues: 124-151 <VAN>
A/Cross-references: UNIPARC:UPI000002B7D3
A/Note: natural and synthetic peptide subjected to kallikrein proteolysis
R/Zivin, R.A.; Condra, J.H.; Dixon, R.A.; Seidman, N.G.; Chretien, M.; Nemer, M.; Chamber
Proc. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984
A/Title: Molecular cloning and characterization of DNA sequences encoding rat and human
A/Reference number: 139458; MUID:85038509; PMID:6238331
A/Accession: 139458
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 119-151, 'RR' <RE2>
A/Cross-references: UNIPARC:UPI000002DD32; GB:K02044; NID:g178631; PIDN:AAA51730.1; PID:
R/Maki, M.; Parmentier, M.; Inagami, T.
Biochem. Biophys. Res. Commun. 125, 797-802, 1984
A/Title: Cloning of genomic DNA for human atrial natriuretic factor.
A/Reference number: 139459; MUID:85096983; PMID:6097248
A/Accession: 139459
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-75 <RE3>
A/Cross-references: UNIPARC:UPI000016A556; GB:K02399; NID:g178633; PIDN:AAA35528.1; PID:
R/Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.; Homcy, C.J.; Duby, A.D.;
Hypertension 7, 31-34, 1985
A/Title: Molecular studies of the atrial natriuretic factor gene.
A/Reference number: 139460
A/Accession: 139460
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-64, 'D', 66-151 <RE4>
A/Cross-references: UNIPARC:UPI000016A557; GB:M54951; NID:g178636; PIDN:AAA35529.1; PID:
R/Greenberg, B.D.; Bensen, G.H.; Selhamer, J.J.; Lewicki, J.A.; Fiddes, J.C.
Nature 312, 656-658, 1984
A/Title: Nucleotide sequence of the gene encoding human atrial natriuretic factor precu
A/Reference number: 137167; MUID:85061627; PMID:6095119
A/Accession: 137167
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 26-151 <RE5>
A/Cross-references: UNIPARC:UPI0000156DAE; EMBL:X01471; NID:g28690; PIDN:CAA25700.1; PID
C/Comment: Cardiodilantin is a vasoconstrictor but not a diuretic or natriuretic.
C/Genetics:
A/Gene: GDB:NPA; ANP; PND
A/Cross-references: GDB:118727; OMIM:108780
A/Map position: 1p36-1p36
A/Introns: 41/3; 150/3
C/Superfamily: natriuretic peptide A precursor
C/Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-151/Product: cardiodilantin #status predicted <CDD>
F:124-151/Product: atrial alpha natriuretic peptide #status experimental <ANP>
F:130-146/Disulfide bonds: #status experimental

Query Match 80.9%; Score 55; DB 1; Length 151;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CFGXXXDRIGXXSXGC 17
Db 130 CFGGRMDRIGAGSLGC 146
RESULT 30
AMBO
Atrial natriuretic peptide precursor - bovine
N/Alternate names: ANP; atrial natriuretic polypeptide
C/Species: Bos primigenius taurus (cattle)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C/Accession: A90124; A93049; A24247; A26090
R/Vlasuk, G.P.; Miller, J.; Bensen, G.H.; Lewicki, J.A.
Biochem. Biophys. Res. Commun. 136, 396-403, 1986
A/Title: Structure and analysis of the bovine atrial natriuretic peptide precursor gen
A/Reference number: A90124; MUID:86215205; PMID:2939830
A/Accession: A90124
A/Molecule type: DNA
A/Residues: 1-152 <VLA>
A/Cross-references: UNIPROT:P07501; UNIPARC:UPI0000125AF7; GB:M13145; NID:g162665; PID
R/ONG, H.; McNICOLL, N.; LAZURE, C.; SEIDMAN, N.; CHRETIEN, M.; CANTIN, M.; DE LEAN, A.
Life Sci. 38, 1309-1315, 1986
A/Title: Purification and sequence determination of bovine atrial natriuretic factor.
A/Reference number: A93049; MUID:86173941; PMID:3007908
A/Accession: A93049
A/Molecule type: protein
A/Residues: 123-150 <ONG>
A/Cross-references: UNIPARC:UPI000002B7D3
C/Genetics:
A/Introns: 40/3; 149/3
C/Superfamily: natriuretic peptide A precursor
C/Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-152/Product: gamma atrial natriuretic factor #status predicted <ANP>
F:123-150/Product: alpha atrial natriuretic peptide #status experimental <ANP>
F:129-145/Disulfide bonds: #status predicted
Query Match 80.9%; Score 55; DB 1; Length 152;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CFGXXXDRIGXXSXGC 17
Db 129 CFGGRMDRIGAGSLGC 145
RESULT 31
AMMS
Atrial natriuretic peptide precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C/Accession: A29370; B43619
R/Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G.
Science 226, 1206-1209, 1984
A/Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.
A/Reference number: A29370; MUID:85065766; PMID:6542248
A/Accession: A29370
A/Molecule type: DNA
A/Residues: 1-152 <SEI>
A/Cross-references: UNIPROT:P05125; UNIPARC:UPI0000027BFB; GB:K02781; NID:g191937; PID
C/Genetics:
A/Introns: 40/3; 149/3
C/Superfamily: natriuretic peptide A precursor
C/Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-150/Product: gamma atrial natriuretic factor #status predicted <ANP>
F:123-150/Product: alpha atrial natriuretic peptide #status predicted <ANP>
F:129-145/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 152;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFCGXXDRIGXXSXGC 17
Db 129 CFCGRIDRIGAGSGLGC 145
RESULT 32
AWRT
atrial natriuretic factor precursor - rat
N;Contains: ANF(1-33); ANF(2-33); ANF(3-33); ANF(8-33); atrial natriuretic peptide; attri
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Feb-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C;Accession: A22570; A01425; A93332; A43617; A93330; A94275; PT0061; A20973; A44190; A60
R;Argentin, S.; Nemer, M.; Drouin, J.; Scott, G.K.; Kennedy, B.P.; Davies, P.L.
J. Biol. Chem. 260, 4568-4571, 1985
A;Title: The gene for rat atrial natriuretic factor.
A;Reference number: A22570; MUID:85182558; PMID:2985557
A;Accession: A22570
A;Molecule type: DNA
A;Residues: 1-152 <ARG>
A;Cross-references: UNIPROT:P01161; UNIPARC:UPI0000125B00; GB:K02062; NID:g202899; PIDN:
R;Yamanaka, M.; Greenberg, B.; Johnson, L.; Seilhamer, J.; Brewer, M.; Friedemann, T.; M
Nature 309, 719-722, 1984
A;Title: Cloning and sequence analysis of the cDNA for the rat atrial natriuretic factor
A;Reference number: A93331; MUID:84219797; PMID:6547210
A;Accession: A01425
A;Molecule type: mRNA
A;Residues: 1-152 <YAM>
A;Cross-references: UNIPARC:UPI0000125B00; EMBL:X00665; NID:g55711; PIDN:CAA25285.1; PID
R;Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.; Tibbells, C.; Inagami, T.
Nature 309, 722-724, 1984
A;Title: Structure of rat atrial natriuretic factor precursor deduced from cDNA sequence
A;Reference number: A93332; MUID:84219798; PMID:6328328
A;Accession: A93332
A;Molecule type: mRNA
A;Residues: 1-152 <MAK>
A;Cross-references: UNIPARC:UPI0000125B00; GB:X00665; EMBL:X00658; NID:g55711; PIDN:CAA2
R;Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, E.; Homcy, C.; Smith, J.A.;
Science 225, 324-326, 1984
A;Title: The structure of rat preproatrial natriuretic factor as defined by a complement
A;Reference number: A43617; MUID:84250178; PMID:6234658
A;Accession: A43617
A;Molecule type: mRNA
A;Residues: 1-152 <SEI>
A;Cross-references: UNIPARC:UPI0000125B00; GB:K02062; GB:K02063; NID:g202899; PIDN:AAA40
R;Atlas, S.A.; Kleiner, H.D.; Camargo, M.J.; Januszewicz, A.; Sealey, J.E.; Larragh, J.H
Nature 309, 717-719, 1984
A;Title: Purification, sequencing and synthesis of natriuretic and vasoactive rat atrial
A;Reference number: A93330; MUID:84219796; PMID:6233494
A;Accession: A93330
A;Molecule type: protein
A;Residues: 126-149 <ATL>
A;Cross-references: UNIPARC:UPI00000351FC
R;Currie, M.G.; Geller, D.M.; Cole, B.R.; Siegel, N.R.; Fok, K.F.; Adams, S.P.; Eubanks,
Science 223, 67-69, 1984
A;Title: Purification and sequence analysis of bioactive atrial peptides (atriopeptins).
A;Reference number: A94275; MUID:84097513; PMID:6419347
A;Accession: A94275
A;Molecule type: protein
A;Residues: 127-149 <CUR>
A;Cross-references: UNIPARC:UPI00000351FB
R;Thibault, G.; Murthy, K.K.; Gutkowska, J.; Seidah, N.G.; Lazure, C.; Chretien, M.; Can
Peptides 9, 47-53, 1988
A;Title: NH2-terminal fragment of rat pro-atrial natriuretic factor in the circulation:
A;Reference number: PT0061; MUID:88203350; PMID:2966345
A;Accession: PT0061
A;Molecule type: protein
A;Residues: 25-28,'X',30-31,'X',33,'X',35-38 <THI>
A;Cross-references: UNIPARC:UPI00001733AA

R;Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia, R.; Cantin, M.; Genest,
Proc. Natl. Acad. Sci. U.S.A. 81, 2640-2644, 1984
A;Title: Amino acid sequence of homologous rat atrial peptides: natriuretic activity of
A;Reference number: A20973; MUID:84194062; PMID:6232612
A;Accession: A20973
A;Molecule type: protein
A;Residues: 118-150 <SE2>
A;Cross-references: UNIPARC:UPI000002BE79
R;Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Bold, M.L.; de Bold, A.J.
Science 228, 323-325, 1985
A;Title: Alignment of rat cardionatrin sequences with the preprocardionatrin sequence fr
A;Reference number: A44190; MUID:85168263; PMID:3157217
A;Accession: A44190
A;Molecule type: mRNA
A;Residues: 1-152 <FLY>
A;Cross-references: UNIPARC:UPI0000125B00; GB:K02062; NID:g202899; PIDN:AAA40735.1; PID
A;Note: part of this sequence, including the amino ends of three mature peptides, was co
R;Belcourt, D.; Varma, D.R.; Toney, K.; Bennett, H.P.J.
Protein Expr. Purif. 1, 28-32, 1990
A;Title: Purification of rat pro-atrial natriuretic factor: a simplified scheme using re
A;Reference number: A60390; MUID:93044510; PMID:2152180
A;Accession: A60390
A;Molecule type: protein
A;Residues: 25-39 <BEL>
A;Cross-references: UNIPARC:UPI00000E66C9
R;Gardner, D.G.; Vlasuk, G.P.; Baxter, J.D.; Fiddes, J.C.; Lewicki, J.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2175-2179, 1987
A;Title: Identification of atrial natriuretic factor gene transcripts in the central ner
A;Reference number: I59094; MUID:87175636; PMID:2951736
A;Accession: I59094
A;Molecule type: mRNA
A;Status: translated from GB/EMBL/DBJ
A;Residues: 38-152 <RES>
A;Cross-references: UNIPARC:UPI0000170882; GB:M15868; NID:g202903; PIDN:AAA40736.1; PID
R;Kangawa, K.; Tawaragi, Y.; Oikawa, S.; Mizuno, A.; Sakuragawa, Y.; Nakazato, H.; Fukud
Nature 312, 152-155, 1984
A;Title: Identification of rat gamma atrial natriuretic polypeptide and characterization
A;Reference number: I58057; MUID:85061500; PMID:6239103
A;Accession: I58057
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-152 <RE2>
A;Cross-references: UNIPARC:UPI0000125B00; EMBL:X01118; NID:g55716; PIDN:CAA25586.1; PID
R;Flynn, T.G.
Can. J. Physiol. Pharmacol. 65, 2013-2020, 1987
A;Title: the elucidation of the structure of atrial natriuretic factor, a new peptide hc
A;Reference number: I52678; MUID:88109092; PMID:2962707
A;Accession: I52678
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-51,'X',53-85,'X',87-152 <RE3>
A;Cross-references: UNIPARC:UPI0000170883; GB:M27498; NID:g202905; PIDN:AAA40737.1; PID
C;Comment: A disulfide bond is required for full activity of atriopetins.
C;Comment: Several active peptides may be derived from the carboxyl region of this prec
C;Genetics:
A;Gene: ANF
A;Introns: 40/3; 149/3
C;Superfamily: natriuretic peptide A precursor
C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-152/Product: pro-atrial natriuretic factor #status experimental <PRO>
F;25-150/Product: cardionatrin IV #status experimental <CN4>
F;25-150/Product: cardionatrin IIV #status experimental <CN3>
F;118-150/Product: ANF(1-33) #status experimental <ANF1>
F;119-150/Product: ANF(2-33) #status experimental <ANF2>
F;120-150/Product: ANF(3-33) #status experimental <ANF3>
F;123-150/Product: cardionatrin I #status experimental <CN1>
F;125-150/Product: ANF(8-33) #status experimental <ANF4>
F;126-150/Product: auriculn B #status experimental <AUB>
F;126-149/Product: auriculn A #status experimental <AUA>
F;127-150/Product: atrial natriuretic factor #status predicted <MAT>
F;127-149/Product: atriopetlin I #status experimental <AT1>
F;127-147/Product: atriopetlin II #status experimental <AT2>

F;129-145/Disulfide bonds: #status experimental

Query Match 80.9%; Score 55; DB 1; Length 152;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| ||
Db 129 CFGGRIDRIGAGSGLGC 145

RESULT 33

AWRB

atrial natriuretic peptide precursor - rabbit
N;Alternate names: ANP; atrial natriuretic polypeptide
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: B25302
R;Okawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato, H.; Matsuo, H.
Biochem. Biophys. Res. Commun. 132, 892-899, 1985
A;Title: Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from complementary DNA
A;Reference number: A90119; MUID:86076957; PMID:2934062
A;Accession: B25302
A;Molecule type: mRNA
A;Residues: 1-153 <OIK>
A;Cross-references: UNIPROT:P07500; UNIPARC:UPI00000125AFE; GB:M12046; NID:g164770; PIDN:
C;Superfamily: natriuretic peptide A precursor
C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-151/Product: gamma atrial natriuretic factor #status predicted <ANF>
F;124-151/Product: alpha atrial natriuretic peptide #status predicted <ANP>
F;130-146/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 153;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| ||
Db 130 CFGGRIDRIGAGSGLGC 146

RESULT 34

S14873

atrial natriuretic peptide precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S14873
R;Maegerl, H.J.; Hanke, M.; Schmeding, G.; Teuteberg, K.; Schulz-Knappe, P.; Forssmann, submitted to the EMBL Data Library, March 1991
A;Reference number: S14872
A;Accession: S14873
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-153 <MAE>
A;Cross-references: UNIPROT:P27104; UNIPARC:UPI00000125AFB; EMBL:X58563; NID:g1008; PIDN:
C;Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 153;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| ||
Db 130 CFGGRMDRIGAGSGLGC 146

RESULT 35

I55480

hypothetical natriuretic peptide/phage fr coat protein mutant fusion protein - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) and phage fr genes engineered and expressed in Escherichia coli
C;Date: 02-Jul-1996 #sequence_revision 05-Sep-1996 #text_change 20-Oct-2000

C;Accession: I55480
R;Berzins, V.; Jansone, I.; Skangals, A.; Kalnins, P.; Liepa, S.; Baumanis, V.
J. Biotechnol. 30, 231-243, 1993
A;Title: High level expression of alpha-human atrial natriuretic factor as a fusion protein
A;Reference number: I55480; MUID:93384792; PMID:7764035
A;Accession: I55480

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-161 <BER>
A;Cross-references: UNIPARC:UPI0000045710; GB:S66567; NID:g435742; PIDN:AAC60713.1; PIDN:
C;Keywords: fusion protein

Query Match 80.9%; Score 55; DB 4; Length 161;
Best Local Similarity 58.8%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
||| ||||| ||
Db 140 CFGGRMDRIGAGSGLGC 156

RESULT 36

AMHUB

natriuretic peptide B precursor [validated] - human
N;Alternate names: brain natriuretic factor-32 (BNF-32); brain natriuretic protein precursor
N;Contents: brain alpha natriuretic peptide; brain gamma natriuretic factor
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: A36736; A30163; A34143; A34661; B34661
R;Seilhamer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki, R.
Biochem. Biophys. Res. Commun. 165, 650-658, 1989
A;Title: Human and canine gene homologs of porcine brain natriuretic peptide.
A;Reference number: A36736; MUID:90088474; PMID:2597152
A;Accession: A36736

A;Molecule type: DNA
A;Residues: 1-134 <SEI>
A;Cross-references: UNIPROT:P16860; UNIPARC:UPI00000350A5; GB:M31776; NID:g179514; PIDN:
R;Sudo, T.; Maekawa, K.; Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 159, 1427-1434, 1989

A;Title: Cloning and sequence analysis of cDNA encoding a precursor for human brain natriuretic peptide
A;Reference number: A30163; MUID:89193743; PMID:2522777
A;Accession: A30163
A;Molecule type: mRNA

A;Residues: 1-134 <SUD>
A;Cross-references: UNIPARC:UPI00000350A5; GB:M31776; NID:g179514; PIDN:AAA35603.1; PDB:1A35603.1
R;Kambayashi, Y.; Nakao, K.; Mukoyama, M.; Saito, Y.; Ogawa, Y.; Shiono, S.; Inouye, K.
FEBS Lett. 259, 341-345, 1990

A;Title: Isolation and sequence determination of human brain natriuretic peptide in human brain
A;Reference number: A34143; MUID:90092577; PMID:2136732
A;Accession: A34143
A;Molecule type: protein

A;Residues: 103-134 <KAM>
A;Cross-references: UNIPARC:UPI00000350A8
R;Hino, J.; Tateyama, H.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 167, 693-700, 1990

A;Title: Isolation and identification of human brain natriuretic peptides in cardiac tissue
A;Reference number: A30161; MUID:90211249; PMID:2138890
A;Accession: A34661

A;Molecule type: protein
A;Residues: 27-58 <HIN>
A;Cross-references: UNIPARC:UPI00001733AB
A;Accession: B34661

A;Molecule type: protein
A;Residues: 103-134 <HT2>
A;Cross-references: UNIPARC:UPI00001733AB
C;Genetics:

A;Gene: GDB:NPPB
A;Cross-references: GDB:127884; OMIM:600295
A;Map position: 1p36-1p36
A;Introns: 44/3; 130/1

C;Superfamily: natriuretic peptide A precursor
C;Keywords: brain; diuretic; hormone; natriuretic; osmoregulation
F;1-26/Domain: signal sequence #status predicted <SIG>

F:27-134/Product: brain gamma natriuretic factor #status experimental <GNF>
F:103-134/Product: brain alpha natriuretic peptide #status experimental <ANF>
F:112-128/Diulfide bonds: #status predicted

Query Match 73.5%; Score 50; DB 1; Length 134;
Best Local Similarity 52.9%; Pred. No. 0.0019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
||| ||| | |||
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 37
A42974

natriuretic peptide, DNP - eastern green mamba
C:Species: Dendroaspis angusticeps (eastern green mamba)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42974
R:Schweitz, H.; Vigne, P.; Moinier, D.; Frelin, C.; Lazdunski, M.
J. Biol. Chem. 267, 13928-13932, 1992
A:Title: A new member of the natriuretic peptide family is present in the venom of the g
A:Reference number: A42974; MUID:92332489; PMID:1352773
A:Accession: A42974
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-38 <SCH>
A:Cross-references: UNIPROT:P28374; UNIPARC:UPI00000350A9
A:Note: sequence extracted from NCBI backbone (NCBIP:108360)
C:Superfamily: natriuretic peptide A precursor

Query Match 70.6%; Score 48; DB 2; Length 38;
Best Local Similarity 52.9%; Pred. No. 0.0017;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
||| ||| | |||
Db 7 CFGHKIDRINHVSNLGC 23

RESULT 38
T18196

pol protein - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18196
R:Takahashi, H.; Okazaki, S.; Fujiwara, H.
Nucleic Acids Res. 25, 1578-1584, 1997
A:Title: A new family of site-specific retrotransposons SAR1, is inserted into telomeri
A:Reference number: Z18809; MUID:97248614; PMID:9092665
A:Accession: T18196
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1067 <TAK>
A:Cross-references: UNIPROT:O01419; UNIPARC:UPI00000756F6; EMBL:D85594; NID:G2055274; PI
C:Superfamily: silkworm pol protein

Query Match 54.4%; Score 37; DB 2; Length 1067;
Best Local Similarity 41.2%; Pred. No. 8.1;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
||| | | | | |
Db 952 CFGRYLMRVGRPHPGC 968

RESULT 39
T34850
probable acid-CoA ligase (EC 6.2.1.-) SC2G5.17 [similarity] - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34850
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, February 1999

A:Reference number: Z21559
A:Accession: T34850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-541 <OLI>
A:Cross-references: UNIPROT:Q9Z5A6; UNIPARC:UPI00000DAECB; EMBL:AL035478; PIDN:CAB36604.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC2G5.17
C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
C:Keywords: acid-thiol ligase
F:70-533/Domain: acetate-CoA ligase homology <ACL>

Query Match 52.9%; Score 36; DB 2; Length 541;
Best Local Similarity 35.3%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
||| | | | | |
Db 239 CFGWVMGNLGTSHGAC 255

RESULT 40
S66859

hypothetical protein YOL160w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O0250
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C:Accession: S66859
R:Gailion, L.; Dujon, B.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66854
A:Accession: S66859
A:Molecule type: DNA
A:Residues: 1-113 <GAI>
A:Cross-references: UNIPROT:Q08321; UNIPARC:UPI000006A9AD; EMBL:Z74902; NID:G1420073; PI
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YOL160w
A:Cross-references: SGD:S0005520
A:Map position: 15L

Query Match 51.5%; Score 35; DB 2; Length 113;
Best Local Similarity 35.3%; Pred. No. 2.9;
Matches 6; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
| : | | | | |
Db 73 CYNVQVSRIGNRKNGC 89

RESULT 41
B44110

mycocerosate synthase (EC 2.3.1.111) - Mycobacterium bovis
C:Species: Mycobacterium bovis
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: B44110
R:Mathur, M.; Kolattukudy, P.E.
J. Biol. Chem. 267, 19388-19395, 1992
A:Title: Molecular cloning and sequencing of the gene for mycocerosic acid synthase, a n
-Guerin.
A:Reference number: A44110; MUID:92406887; PMID:1527058
A:Accession: B44110
A:Molecule type: DNA; protein
A:Residues: 1-2110 <MAT>
A:Cross-references: UNIPROT:Q02251; UNIPARC:UPI000012ED5D; GB:M95808; NID:G149977; PIDN:
A:Note: sequence extracted from NCBI backbone (NCBIN:113897, NCBIP:113899)
A:Note: the source is designated as Mycobacterium tuberculosis var. bovis Bacillus Calme
C:Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I ho
nase homology; [acyl-carrier-protein] S-malonyltransferase homology
C:Keywords: acyltransferase; carrier protein; coenzyme A; phosphotransferase
F:27-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F;534-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1443-1732/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;1764-1944/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;2015-2095/Domain: acyl carrier protein homology <ACPl>

Query Match 51.5%; Score 35; DB 2; Length 2110;
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 7 DRIGXXSXXGC 17
||:| | ||
Db 1501 DRVGFSSEGC 1511

RESULT 42

A70668

mycocerosate synthase (EC 2.3.1.111) - Mycobacterium tuberculosis

C/Species: Mycobacterium tuberculosis

C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C/Accession: A70668

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: A70668

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-2111 <COL>

A;Cross-references: UNIPROT:P96291; UNIPARC:UPI0000036BA0; GB:Z83858; GB:AL123456; NID:9

A;Experimental source: strain H37Rv

C/Genetics:

A;Gene: mas

C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I nd

nase homology; [acyl-carrier-protein] S-malonyltransferase homology

C;Keywords: acyltransferase; carrier protein; coenzyme A; phosphotransferase

F;27-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F;534-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

F;1444-1733/Domain: long-chain alcohol dehydrogenase homology <LADH>

F;1765-1945/Domain: short-chain alcohol dehydrogenase homology <SADH>

F;2016-2096/Domain: acyl carrier protein homology <ACPl>

Query Match 51.5%; Score 35; DB 2; Length 2111;
Best Local Similarity 54.5%; Pred. No. 41;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 7 DRIGXXSXXGC 17
||:| | ||
Db 1502 DRVGFSSEGC 1512

RESULT 43

C86926

probable mycocerosic synthase [imported] - Mycobacterium leprae

C/Species: Mycobacterium leprae

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C/Accession: C86926

R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: C86926

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-2116 <STO>

A;Cross-references: UNIPROT:Q9CD78; UNIPARC:UPI00000C6C57; GB:AL450380; NID:G13092517; F

C;Genetics:

A;Gene: mas

C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I nase homology; [acyl-carrier-protein] S-malonyltransferase homology

C;Keywords: carrier protein

Query Match 51.5%; Score 35; DB 2; Length 2116;
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 7 DRIGXXSXXGC 17
||:| | ||
Db 1500 DRVGFSSEGC 1510

RESULT 44

S72705

mycocerosate synthase (EC 2.3.1.111) - Mycobacterium leprae

N/Alternate names: Lepb1170_C2_209 protein

C/Species: Mycobacterium leprae

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S72705

R;Smith, D.R.; Robison, K.

Submitted to the EMBL Data Library, November 1993

A;Description: Mycobacterium leprae cosmid B1170.

A;Reference number: S72693

A;Accession: S72705

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-2118 <SMI>

A;Cross-references: UNIPROT:Q49624; UNIPARC:UPI00000CA943; EMBL:U00010; NID:G466780; P

C/Genetics:

A;Start codon: TTG

C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I ;

nase homology; [acyl-carrier-protein] S-malonyltransferase homology

C;Keywords: acyltransferase; carrier protein; coenzyme A

F;28-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F;536-816/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

F;1449-1738/Domain: long-chain alcohol dehydrogenase homology <LADH>

F;1770-1954/Domain: short-chain alcohol dehydrogenase homology <SADH>

F;2038-2110/Domain: acyl carrier protein homology <ACPl>

Query Match 51.5%; Score 35; DB 2; Length 2118;
Best Local Similarity 54.5%; Pred. No. 41;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 7 DRIGXXSXXGC 17
||:| | ||
Db 1507 DRVGVSRRNC 1517

RESULT 45

A11422

hypothetical protein bvrC [imported] - Listeria monocytogenes (strain EGD-e)

C/Species: Listeria monocytogenes

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: A11422

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeck, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, I D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; r

ok, C.; Schluter, T.; Simoes, N.; Tietrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlan

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: A11422

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-327 <GLA>

A;Cross-references: UNIPROT:Q8Y3P8; UNIPARC:UPI00000556DD; GB:NC_003210; PIDN:CAD00999

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: bvrC

C;Superfamily: ADP-ribosylglycohydrolase

Query Match		50.0%;	Score 34;	DB 2;	Length 327;			
Best Local Similarity		41.2%;	Pred. No. 13;					
Matches		7;	Conservative	0;	Mismatches 10; Indels 0; Gaps 0;			
OY	1	CFGXXXDRIGXXSXGC 17						
Db	276	CIGWDTDTTIGAISAGIC 292						
RESULT 46								
H97462								
hypothetical protein AGR_C_1553 [imported] - Agrobacterium tumefaciens (strain C58, Cere								
C;Species: Agrobacterium tumefaciens								
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004								
C;Accession: H97462								
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirollo, B.; Goldman,								
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;								
Science 294, 2323-2328, 2001								
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum								
A;Reference number: A97359; MUID:21608551; PMID:11743194								
A;Accession: H97462								
A;Status: preliminary								
A;Molecule type: DNA								
A;Residues: 1-504 <KUR>								
A;Cross-references: UNIPROT:Q8UH35; UNIPARC:UPI00000D1953; GB:AE007869; PIDN:AAK86657.1;								
C;Genetics:								
A;Gene: AGR_C_1553								
A;Map position: circular chromosome								
Query Match		50.0%;	Score 34;	DB 2;	Length 504;			
Best Local Similarity		54.5%;	Pred. No. 18;					
Matches		6;	Conservative	1;	Mismatches 4; Indels 0; Gaps 0;			
OY	7	DRIGXXSXGC 17						
Db	29	DRIGVANGC 39						
RESULT 47								
S50856								
Whn protein - rat								
C;Species: Rattus norvegicus (Norway rat)								
C;Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004								
C;Accession: S50856								
R;Nehls, M.; Pfeifer, D.; Schorpp, M.; Hedrich, H.; Boehm, T.								
Nature 372, 103-107, 1994								
A;Title: New member of the winged-helix protein family disrupted in mouse and rat nude r								
A;Reference number: S50856; MUID:95059376; PMID:7969402								
A;Accession: S50856								
A;Status: preliminary								
A;Molecule type: mRNA								
A;Residues: 1-648 <NEH>								
A;Cross-references: UNIPARC:UPI0000020C07; GB:X81593; NID:G563511; PIDN:CA57279.1; PID:								
F;271-364/Domain: fork head DNA-binding domain homology <FHD>								
Query Match		50.0%;	Score 34;	DB 2;	Length 648;			
Best Local Similarity		35.3%;	Pred. No. 23;					
Matches		6;	Conservative	2;	Mismatches 9; Indels 0; Gaps 0;			
OY	1	CFGXXXDRIGXXSXGC 17						
Db	328	CFEKENKSGSSSRKGC 344						
RESULT 48								
H70819								
probable polyketide synthase - Mycobacterium tuberculosis (strain H37RV)								
C;Species: Mycobacterium tuberculosis								
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004								
C;Accession: H70819								
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.								
; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.								
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.								

Nature 393, 537-544, 1998					
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.					
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome					
A;Reference number: A70500; MUID:98295987; PMID:9634230					
A;Accession: H70819					
A;Status: preliminary; nucleic acid sequence not shown; translation not shown					
A;Molecule type: DNA					
A;Residues: 1-2108 <COL>					
A;Cross-references: UNIPROT:O53901; UNIPARC:UPI00000D3B08; GB:AL022000; GB:AL123456; NID					
A;Experimental source: strain H37Rv					
C;Genetics:					
A;Gene: pks5					
C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I ho					
nase homology; [acyl-carrier-protein] S-malonyltransferase homology					
C;Keywords: carrier protein					
F;36-434/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>					
F;546-826/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>					
F;1444-1733/Domain: long-chain alcohol dehydrogenase homology <LADH>					
F;1765-1945/Domain: short-chain alcohol dehydrogenase homology <SADH>					
F;2029-2094/Domain: acyl carrier protein homology <ACP1>					
OY					
7 DRIGXXSXGC 17					
:					
Db 1502 DRVGMSPNGC 1512					
RESULT 49					
A97088					
uncharacterized protein, homolog of PHNB E.coli [imported] - Clostridium acetobutylicum					
C;Species: Clostridium acetobutylicum					
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004					
C;Accession: A97088					
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,					
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.					
J. Bacteriol. 183, 4823-4838, 2001					
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo					
A;Reference number: A96900; MUID:21359325; PMID:21359325					
A;Accession: A97088					
A;Status: preliminary					
A;Molecule type: DNA					
A;Residues: 1-137 <KUR>					
A;Cross-references: UNIPROT:Q971W5; UNIPARC:UPI00000CA223; GB:AE001437; PIDN:AAK79492.1;					
A;Experimental source: Clostridium acetobutylicum ATCC824					
C;Genetics:					
A;Gene: CAC1525					
OY					
1 CFGXXXDRIGXXSXGC 17					
:					
Db 119 CYGSLTDKFGIEWHFNC 135					
RESULT 50					
T10652					
hypothetical protein T5F17.30 - Arabidopsis thaliana					
C;Species: Arabidopsis thaliana (mouse-ear cress)					
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004					
C;Accession: T10652					
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro					
submitted to the Protein Sequence Database, June 1999					
A;Reference number: Z16533					
A;Accession: T10652					
A;Molecule type: DNA					
A;Residues: 1-419 <BEV>					
A;Cross-references: UNIPROT:Q9M0H3; UNIPARC:UPI00000A7272; EMBL:AL049917; GSPDB:GN000062,					
A;Experimental source: cultivar Columbia; BAC clone T5F17					

C;Genetics:
A;Gene: ATSP.T5F17.30

A;Map position: 4

A;Introns: 97/1; 243/3; 328/3

C;Superfamily: Arabidopsis thaliana hypothetical protein F17J16.20

Query Match 48.5%; Score 33; DB 2; Length 419;
Best Local Similarity 35.3%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
Db 53 CLWTRFDRTGFMEVAGC 69

Search completed: January 26, 2006, 14:45:29
Job time : 23 secs

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